

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 17, 2005, 09:51:36 ; Search time 39.4398 Seconds
(without alignments)
1118.605 Million cell updates/sec

Title: US-10-725-121A-103

Perfect score: 3090
Sequence: 1 MFGRKKRVEISAPSNFHEH.....LAXAGPPASIVLMRNRTR 591

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA: *
1: /cgn2_6/ptodata/1/1aa/5A_COMB.pep: *
2: /cgn2_6/ptodata/1/1aa/5B_COMB.pep: *
3: /cgn2_6/ptodata/1/1aa/6A_COMB.pep: *
4: /cgn2_6/ptodata/1/1aa/6B_COMB.pep: *
5: /cgn2_6/ptodata/1/1aa/PCTUS_COMB.pep: *
6: /cgn2_6/ptodata/1/1aa/backfile1.pep: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|--------|-------------|--------|-------|---------------------|
| 1 | 3090 | 100.0 | 591 | 3 | US-09-082-737-2 |
| 2 | 3090 | 100.0 | 591 | 4 | US-09-688-188B-103 |
| 3 | 3090 | 100.0 | 591 | 4 | US-09-718-032-2 |
| 4 | 3090 | 100.0 | 591 | 4 | US-09-291-417D-103 |
| 5 | 3090 | 100.0 | 591 | 4 | US-09-949-016-6665 |
| 6 | 3090 | 100.0 | 620 | 4 | US-09-949-016-7206 |
| 7 | 2073 | 67.1 | 398 | 4 | US-09-688-188B-30 |
| 8 | 2073 | 67.1 | 398 | 4 | US-09-291-417D-30 |
| 9 | 1473.5 | 47.7 | 681 | 4 | US-09-688-188B-29 |
| 10 | 1473.5 | 47.7 | 681 | 4 | US-09-291-417D-29 |
| 11 | 1473.5 | 47.6 | 694 | 4 | US-09-949-016-10445 |
| 12 | 1470.5 | 47.6 | 681 | 4 | US-09-765-815-2 |
| 13 | 1277 | 41.3 | 250 | 3 | US-09-082-737-3 |
| 14 | 1277 | 41.3 | 250 | 3 | US-09-718-032-3 |
| 15 | 912 | 29.5 | 544 | 2 | US-08-935-760-2 |
| 16 | 909 | 29.4 | 544 | 4 | US-09-949-016-11562 |
| 17 | 907 | 29.4 | 544 | 4 | US-09-688-188B-95 |
| 18 | 907 | 29.4 | 544 | 4 | US-09-291-417D-95 |
| 19 | 904 | 29.3 | 524 | 4 | US-09-538-092-1301 |
| 20 | 900 | 29.1 | 524 | 4 | US-08-615-942A-2 |
| 21 | 900 | 29.1 | 524 | 4 | US-09-237-325-2 |
| 22 | 899 | 29.1 | 544 | 3 | US-08-559-397A-19 |
| 23 | 894 | 28.9 | 506 | 1 | US-08-475-682-2 |
| 24 | 894 | 28.9 | 506 | 1 | US-08-780-833-2 |
| 25 | 894 | 28.9 | 506 | 1 | US-08-636-036-2 |
| 26 | 894 | 28.9 | 506 | 1 | US-08-918-509-2 |
| 27 | 894 | 28.9 | 506 | 3 | US-08-918-509-2 |

| | | | | | | |
|----|-------|------|-----|---|----------------------|-------------------|
| 28 | 894 | 28.9 | 506 | 3 | US-09-108-262-2 | Sequence 2, Appl |
| 29 | 894 | 28.9 | 506 | 4 | US-09-688-188B-94 | Sequence 94, Appl |
| 30 | 894 | 28.9 | 506 | 4 | US-09-291-417D-94 | Sequence 10951, A |
| 31 | 893.5 | 28.9 | 551 | 4 | US-09-949-016-10951 | Sequence 10951, A |
| 32 | 892.5 | 28.9 | 545 | 4 | US-09-538-092-1297 | Sequence 4, Appl |
| 33 | 891.5 | 28.9 | 545 | 2 | US-08-935-760-4 | Sequence 93, Appl |
| 34 | 891.5 | 28.9 | 545 | 4 | US-09-688-188B-93 | Sequence 93, Appl |
| 35 | 891.5 | 28.9 | 545 | 4 | US-09-291-417D-93 | Sequence 29, Appl |
| 36 | 867 | 28.1 | 544 | 3 | US-08-559-397A-30 | Sequence 30, Appl |
| 37 | 849 | 27.5 | 544 | 3 | US-08-559-397A-30 | Sequence 2, Appl |
| 38 | 833.5 | 27.0 | 465 | 2 | US-08-114-555A-2 | Sequence 31, Appl |
| 39 | 821 | 26.6 | 465 | 3 | US-08-559-397A-31 | Sequence 2, Appl |
| 40 | 814.5 | 26.4 | 465 | 3 | US-08-559-397A-2 | Sequence 10, Appl |
| 41 | 804 | 26.0 | 305 | 4 | US-09-765-815-10 | Sequence 2, Appl |
| 42 | 782 | 25.3 | 793 | 3 | US-09-588-256-10 | Sequence 3, Appl |
| 43 | 769 | 24.9 | 268 | 2 | US-08-852-743-3 | Sequence 3, Appl |
| 44 | 769 | 24.9 | 268 | 3 | US-09-185-370-3 | Sequence 3, Appl |
| 45 | 755 | 24.4 | 410 | 4 | US-09-248-796A-18461 | Sequence 18461, A |

ALIGNMENTS

```

RESULT 1
US-09-082-737-2
; Sequence 2, Application US/09082737
; Patent No. 6013500
;
GENERAL INFORMATION:
; APPLICANT: Minden, Audrey
; TITLE OF INVENTION: PAK1 A No. 6013500e1 Gene Encoding A Serine/
; TITLE OF INVENTION: Threonine Kinase
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Cooper & Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 11230
;
COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/082,737
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 0575/55311
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 278-0400
; TELEFAX: (212) 391-0525
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 591 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-082-737-2
;
Query Match 100.0%; Score 3090; DB 3; Length 591;
Best Local Similarity 100.0%; Pred. No. 3e-191;
Matches 591; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
QY 1 MFGRKKRVEISAPSNFHEHVTGPDHOKPTGLPRQMSLIRSSARRKPLVDPACIT 60
Db 1 MFGRKKRVEISAPSNFHEHVTGPDHOKPTGLPRQMSLIRSSARRKPLVDPACIT 60
QY 61 STOPGPKTTIVGSKAGKGLTLIDDFRNNSVTSNLSIRRSPPPPARAQDNQMPER 120

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Db 121 PATTARAGPGKAGSRGRFAGHSBAGGSGDRBRAGPEKPKSSRBSGSGPQESSRDRLPL 180
QY 181 SGPDVGTPOGAGLASGAKLAAGRPNNTYPRADTDHPSRGAQGBPHDVAENGPASAGLAIIP 240
Db 181 SGPDVGTPOGAGLASGAKLAAGRPNNTYPRADTDHPSRGAQGBPHDVAENGPASAGLAIIP 240
QY 241 QSSSSSRPPTRRARGAPSPGVLGPHASBPOLAPACTPAPAVPGPPGPSPOREPORVS 300
Db 241 QSSSSSRPPTRRARGAPSPGVLGPHASBPOLAPACTPAPAVPGPPGPSPOREPORVS 300
QY 301 HEQFRALQVLDVDPGDRSYLDNFIKIGSGSTGIVCIATVRSSGKLVAVKMDLRKQORR 360
Db 301 HEQFRALQVLDVDPGDRSYLDNFIKIGSGSTGIVCIATVRSSGKLVAVKMDLRKQORR 360
QY 361 ELLFNEVIMRDYOHENNVEMNYSYLVGDELMVMEELBEGALTDIYTHTRMNEBOJIAAV 420
Db 361 ELLFNEVIMRDYOHENNVEMNYSYLVGDELMVMEELBEGALTDIYTHTRMNEBOJIAAV 420
QY 421 CLAVLOALSTVLAQGVITHRDIKSDSILLTDGRVKLSDFGFCQVSKVPRKSLVGTPTY 480
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Db 541 VSPSLKGFILDRLLVDRPAQRATAELKHPFLAKAGPPASIVPLMRONRTR 591

RESULT 2
US-09-688-188B-103
Sequence 103, Application US/09688188B
Patent No. 6656716
GENERAL INFORMATION:
APPLICANT: PIOMMAN, GREGORY
APPLICANT: MARTINEZ, RICARDO
TITLE OF INVENTION: STEZO-RELATED PROTEIN KINASES
FILE REFERENCE: 0386502/0328
CURRENT APPLICATION NUMBER: US/09/688,188B
CURRENT FILING DATE: 2000-10-16
PRIOR APPLICATION NUMBER: 09/291,417
PRIOR FILING DATE: 1999-04-14
PRIOR APPLICATION NUMBER: 60/081,784
PRIOR FILING DATE: 1998-04-14
NUMBER OF SEQ ID NOS: 155
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 103
LENGTH: 591
TYPE: PRT
ORGANISM: Homo sapiens
US-09-688-188B-103

Query Match 100.0%; Score 3090; DB 4; Length 591;
Best Local Similarity 100.0%; Pred. No. 3e-191;
Matches 591; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MFGKRRKRVIEISAPSNFHRVHTGPDQHEOKFTGLPRQOSLIBSARBRKPLVDPACIT 60
Db 1 MFGKRRKRVIEISAPSNFHRVHTGPDQHEOKFTGLPRQOSLIBSARBRKPLVDPACIT 60
QY 61 S10GAPKTIIVGSGKAGKADGAL.TLLDDEFENMSVTRNSILNRDSDPPPARARQENGMPEE 120
Db 61 S10GAPKTIIVGSGKAGKADGAL.TLLDDEFENMSVTRNSILNRDSDPPPARARQENGMPEE 120
QY 121 PATTARAGPGKAGSRGRFAGHSBAGGSGDRBRAGPEKPKSSRBSGSGPQESSRDRLPL 180
Db 121 PATTARAGPGKAGSRGRFAGHSBAGGSGDRBRAGPEKPKSSRBSGSGPQESSRDRLPL 180

Db 121 PATTARAGPGKAGSRGRFAGHSBAGGSGDRBRAGPEKPKSSRBSGSGPQESSRDRLPL 180
QY 181 SGPDVGTPOGAGLASGAKLAAGRPNNTYPRADTDHPSRGAQGBPHDVAENGPASAGLAIIP 240
Db 181 SGPDVGTPOGAGLASGAKLAAGRPNNTYPRADTDHPSRGAQGBPHDVAENGPASAGLAIIP 240
QY 241 QSSSSSRPPTRRARGAPSPGVLGPHASBPOLAPACTPAPAVPGPPGPSPOREPORVS 300
Db 241 QSSSSSRPPTRRARGAPSPGVLGPHASBPOLAPACTPAPAVPGPPGPSPOREPORVS 300
QY 301 HEQFRALQVLDVDPGDRSYLDNFIKIGSGSTGIVCIATVRSSGKLVAVKMDLRKQORR 360
Db 301 HEQFRALQVLDVDPGDRSYLDNFIKIGSGSTGIVCIATVRSSGKLVAVKMDLRKQORR 360
QY 361 ELLFNEVIMRDYOHENNVEMNYSYLVGDELMVMEELBEGALTDIYTHTRMNEBOJIAAV 420
Db 361 ELLFNEVIMRDYOHENNVEMNYSYLVGDELMVMEELBEGALTDIYTHTRMNEBOJIAAV 420
QY 421 CLAVLOALSTVLAQGVITHRDIKSDSILLTDGRVKLSDFGFCQVSKVPRKSLVGTPTY 480
Db 421 CLAVLOALSTVLAQGVITHRDIKSDSILLTDGRVKLSDFGFCQVSKVPRKSLVGTPTY 480
QY 481 WMAPBELISRLPYGPBYDVIMSLGIMVLEMVDGEBPYFNBEPPLKAMKMI RDNLPPRLKNYLHK 540
Db 481 WMAPBELISRLPYGPBYDVIMSLGIMVLEMVDGEBPYFNBEPPLKAMKMI RDNLPPRLKNYLHK 540
QY 541 VSPSLKGFILDRLLVDRPAQRATAELKHPFLAKAGPPASIVPLMRONRTR 591
Db 541 VSPSLKGFILDRLLVDRPAQRATAELKHPFLAKAGPPASIVPLMRONRTR 591

RESULT 3
US-09-718-032-2
Sequence 2, Application US/09718032
Patent No. 6667168
GENERAL INFORMATION:
APPLICANT: The Trustees of Columbia University
APPLICANT: Minden, Audrey
TITLE OF INVENTION: PAK, A NOVEL GENE ENCODING A SERINE/THREONINE KINASE
FILE REFERENCE: 575/55311-A-PCT-US
CURRENT APPLICATION NUMBER: US/09/718,032
CURRENT FILING DATE: 2000-11-21
PRIOR APPLICATION NUMBER: PCT/US99/11341
PRIOR FILING DATE: 1999-05-21
PRIOR APPLICATION NUMBER: 09/082,737
PRIOR FILING DATE: 1998-05-21
NUMBER OF SEQ ID NOS: 17
SOFTWARE: PatentIn version 3.1
SEQ ID NO 2
LENGTH: 591
TYPE: PRT
ORGANISM: human
US-09-718-032-2

Query Match 100.0%; Score 3090; DB 4; Length 591;
Best Local Similarity 100.0%; Pred. No. 3e-191;
Matches 591; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MFGKRRKRVIEISAPSNFHRVHTGPDQHEOKFTGLPRQOSLIBSARBRKPLVDPACIT 60
Db 1 MFGKRRKRVIEISAPSNFHRVHTGPDQHEOKFTGLPRQOSLIBSARBRKPLVDPACIT 60
QY 61 S10GAPKTIIVGSGKAGKADGAL.TLLDDEFENMSVTRNSILNRDSDPPPARARQENGMPEE 120
Db 61 S10GAPKTIIVGSGKAGKADGAL.TLLDDEFENMSVTRNSILNRDSDPPPARARQENGMPEE 120
QY 121 PATTARAGPGKAGSRGRFAGHSBAGGSGDRBRAGPEKPKSSRBSGSGPQESSRDRLPL 180
Db 121 PATTARAGPGKAGSRGRFAGHSBAGGSGDRBRAGPEKPKSSRBSGSGPQESSRDRLPL 180
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Db 181 SGPDVGTPOGAGLASGAKLAAGRPNNTYPRADTDHPSRGAQGBPHDVAENGPASAGLAIIP 240



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Protein Sequence Searches - February 2005

All of the sequence databases on ABSS have recently been updated.

- Please note that the curators of the UniProt database have purged some temporary accession numbers from the most recent version of UniProt. These sequences have been assigned new permanent accession numbers. The new UniProt record may not contain the previous temporary accession number.
- If you encounter an accession number from an older search run against UniProt (results file extension **.rup**) that can no longer be found in the database, the permanent record with the new accession number can be found by searching the old accession number in the UniProt Protein Archive database (UniPARC) at:

<http://www.pir.uniprot.org/database/archive.shtml>

If you have any questions regarding this information or your results, please contact any STIC searcher.

When submitting sequence search results for scanning into IFW, please include a copy of this attachment to assist any future Examiners or members of the public who may encounter UniProt temporary accession numbers.

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OM protein - protein search, using sw model

Run on: November 17, 2005, 10:09:48 / Search time 92.1557 Seconds
(without alignments)
2211.556 Million cell updates/sec

Title: US-10-725-121A-30

Sequence: 1 ASGAKLAAGPFTYPPADT.....LAKAGPPASIVPLKQRNTR 398

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues
Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UnlProt 03:.*
1: unlProt_sprot:.*
2: unlProt_trembl:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|--------|-------------|--------|-------|-------------|
| 1 | 2073 | 100.0 | 591 | 1 | PAK4_HUMAN |
| 2 | 1963 | 94.7 | 407 | 1 | Q8K0U2 |
| 3 | 1963 | 94.7 | 593 | 1 | PAK4_MOUSE |
| 4 | 1963 | 94.7 | 597 | 2 | Q6ZPX0 |
| 5 | 1953 | 94.2 | 593 | 2 | Q80297 |
| 6 | 1926 | 92.9 | 501 | 2 | Q8N4E1 |
| 7 | 1925 | 92.9 | 438 | 2 | Q8NDE3 |
| 8 | 1925 | 92.9 | 467 | 2 | Q9ULS8 |
| 9 | 1612.5 | 77.8 | 650 | 2 | Q90W62 |
| 10 | 1586 | 76.5 | 663 | 2 | Q6GM11 |
| 11 | 1351 | 65.2 | 719 | 2 | Q8C015 |
| 12 | 1343 | 64.8 | 719 | 2 | Q8BVB0 |
| 13 | 1340 | 64.6 | 719 | 1 | PAK7_HUMAN |
| 14 | 1340 | 64.6 | 719 | 2 | Q8TB53 |
| 15 | 1339.5 | 64.6 | 711 | 2 | Q6NV04 |
| 16 | 1333 | 64.3 | 719 | 2 | Q6RW57 |
| 17 | 1259.5 | 60.8 | 639 | 1 | PAKM_DROME |
| 18 | 1241 | 59.9 | 540 | 2 | Q8NC55 |
| 19 | 1237.5 | 59.7 | 558 | 2 | Q7QCS5 |
| 20 | 1197 | 57.7 | 681 | 1 | PAK6_HUMAN |
| 21 | 1160 | 56.0 | 229 | 2 | Q9CS71 |
| 22 | 911.5 | 44.0 | 540 | 2 | Q9U3M1 |
| 23 | 911.5 | 44.0 | 542 | 2 | Q18637 |
| 24 | 856 | 41.3 | 704 | 2 | Q24190 |
| 25 | 856 | 41.3 | 704 | 2 | Q9V113 |
| 26 | 851 | 41.1 | 704 | 2 | Q24213 |
| 27 | 843 | 40.7 | 559 | 1 | PAK3_HUMAN |
| 28 | 843 | 40.7 | 559 | 1 | PAK3_PANTR |
| 29 | 843 | 40.7 | 559 | 1 | PAK3_PONPY |
| 30 | 842 | 40.6 | 524 | 1 | PAK2_HUMAN |
| 31 | 838 | 40.4 | 704 | 2 | Q7QD76 |

| RESULT 1 | PAK4_HUMAN | STANDARD; | PRT; | 591 AA. |
|----------|---|-----------|------|---------|
| AC | Q96013; Q9BUJ3; | | | |
| DT | 16-OCT-2001 (Rel. 40, Created) | | | |
| DT | 16-OCT-2001 (Rel. 40, Last sequence update) | | | |
| DT | 05-JUL-2004 (Rel. 44, Last annotation update) | | | |
| DE | Serine/threonine-protein kinase PAK 4 (EC 2.7.1.37) (p21-activated kinase 4) (PAK-4). | | | |
| GN | Name=PAK4; | | | |
| OS | Homo sapiens (Human). | | | |
| OC | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; | | | |
| OC | Mammalia; Butcheria; Primates; Carnivora; Hominoidea; Homo. | | | |
| OX | NCBI_TaxID=9606; | | | |
| RN | [1] | | | |
| RP | SEQUENCE FROM N.A. (ISOFORM 1). | | | |
| RX | MEDLINE=99043860; PubMed=9822598; DOI=10.1093/emboj/17.22.6527; | | | |
| RA | Abo A., Qu J., Camarano M.S., Dan C., Fritsch A., Baud V., | | | |
| RT | Belisle B., Minden A., | | | |
| RT | "PAK4", a novel effector for Cdc42Hs, is implicated in the reorganization of the actin cytoskeleton and in the formation of filopodia." | | | |
| RT | EMBO J. 17:6527-6540(1998). | | | |
| RL | [2] | | | |
| RN | SEQUENCE FROM N.A. (ISOFORM 1). | | | |
| RP | Meinick M.B.; | | | |
| RA | Submitted (MAY-1997) to the EMBL/Genbank/DBJ databases. | | | |
| RN | [3] | | | |
| RP | SEQUENCE FROM N.A. (ISOFORMS 1 AND 2). | | | |
| RC | TISSUE=Eye, Pancreas, and Placenta; | | | |
| RX | MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899; | | | |
| RA | Klausner R.D., Collins F.S., Wagner L., Sherman C.M., Schuler G.D., | | | |
| RA | Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., | | | |
| RA | Hopkins R.P., Jordan H., Moore T., Max S.I., Wang J., Heit F., | | | |
| RA | Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., | | | |
| RA | Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., | | | |
| RA | Brownstein M.J., Udell T.B., Toshiyuki S., Cavatini P., Prange C., | | | |
| RA | Rata S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J., | | | |
| RA | Boak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., | | | |
| RA | Butterfield Y.S.N., Krzyzanski M.I., Skalka U., Smallus D.E., | | | |
| RA | Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., | | | |
| RA | Falley J., Helton B., Kettelman M., Madan A., Rodriguez S., Sanchez A., | | | |
| RA | Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., | | | |
| RA | Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C., | | | |
| RA | Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., | | | |
| RA | Butterfield Y.S.N., Krzyzanski M.I., Skalka U., Smallus D.E., | | | |
| RA | Schneerch A., Schein J.E., Jones S.J.M., Marra M.A., | | | |
| RT | "Generation and Initial Analysis of more than 15,000 full-length human and mouse cDNA sequences." | | | |
| RT | Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002). | | | |
| CC | -1- FUNCTION: Activates the JNK pathway. Implicated in the reorganization of the actin cytoskeleton and in the formation of filopodia. | | | |

| | | | | | | |
|----|-------|------|-----|---|------------|---------------------|
| 32 | 833.5 | 40.2 | 524 | 2 | Q6ISG3 | Q6ISG3 homo sapien |
| 33 | 832.5 | 40.2 | 544 | 1 | PAK3_RAT | Q62828 rattus norv |
| 34 | 832.5 | 40.2 | 544 | 2 | Q8K1K6 | Q8K1K6 mus musculu |
| 35 | 832.5 | 40.2 | 559 | 1 | PAK3_MOUSE | Q61036 mus musculu |
| 36 | 829.5 | 40.0 | 524 | 1 | PAK2_MOUSE | Q6C143 mus musculu |
| 37 | 829.5 | 40.0 | 524 | 1 | PAK2_RAT | Q64303 rattus norv |
| 38 | 828.5 | 40.0 | 524 | 2 | Q9OYT0 | Q9OYT0 rattus norv |
| 39 | 827.5 | 39.9 | 564 | 2 | Q8AXB4 | Q8AXB4 xenopus lae |
| 40 | 825 | 39.8 | 524 | 1 | PAK2_RABIT | Q29502 oryctolagus |
| 41 | 822 | 39.7 | 517 | 2 | Q6DG42 | Q6DG42 brachydantio |
| 42 | 822 | 39.7 | 517 | 2 | Q8AW67 | Q8AW67 brachydantio |
| 43 | 817.5 | 39.4 | 545 | 1 | PAK1_HUMAN | Q13153 homo sapien |
| 44 | 817 | 39.4 | 544 | 1 | PAK1_RAT | P35465 rattus norv |
| 45 | 817 | 39.4 | 577 | 2 | Q803Z0 | Q803Z0 brachydantio |

```

CC -1- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC -1- SUBUNIT: Interacts tightly with GTP-bound but not GPP-bound
CC CDCA2/p21 and weakly with RAC1.
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=1;
CC IsoId=O96013-1; Sequence=Displayed;
CC Name=2;
CC IsoId=O96013-2; Sequence=VSP_004892, VSP_004893;
CC Note=No experimental confirmation available;
CC -1- TISSUE SPECIFICITY: Highest expression in prostate, testis and
CC colon.
CC -1- PTM: Autophosphorylated when activated by CDCA2/p21.
CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family. STE20
CC subfamily.
CC -1- SIMILARITY: Contains 1 CRIB domain.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by, and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AJ011855; CAA09820.1; -
DR EMBL; AF005046; AAD01210.1; -
DR EMBL; BC002921; AAH02921.1; -
DR EMBL; BC011368; AAH11368.1; -
DR EMBL; BC025282; AAH25282.1; -
DR HSSP; Q13153; 1F3M.
DR Genew; HGNC:16059; PAK4.
DR H-invDB; HIX0015110; -.
DR MIM; 605451; -.
DR GO; GO:0005794; C:Golgi apparatus; TAS.
DR GO; GO:0006928; P:cell motility; TAS.
DR GO; GO:0007165; P:signal transduction; TAS.
DR Interpro; IPR011009; Kinase like.
DR Interpro; IPR000095; PAKbox/ehobind.
DR Interpro; IPR000719; Prot kinase.
DR Interpro; IPR008271; Ser_thr_kin_AS.
DR Interpro; IPR002290; Ser_thr_pkinase.
DR Interpro; IPR011026; WASP_C.
DR Pfam; PF00786; PBD; 1.
DR Pfam; PF00069; Pkinase; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00285; PBD; 1.
DR SMART; SM00220; S_TKC; 1.
DR PROSITE; PS0108; CRIB; 1.
DR PROSITE; PS0107; PROTEIN KINASE ATP; 1.
DR PROSITE; PS0011; PROTEIN KINASE DOM; 1.
DR PROSITE; PS00108; PROTEIN KINASE_ST; FALSE_NEG.
KW Alternative splicing; ATP-binding; Phosphorylation;
KW Serine/threonine-protein kinase; Transferase.
FT DOMAIN 11 24
FT DOMAIN 25 320
FT DOMAIN 321 572
FT NP_BIND 327 335
FT BINDING 350 350
FT ACT_SITE 440 440
FT VARSPIC 120 120
FT VARSPIC 121 285
FT FTID=VSP_004892.
FT FTID=VSP_004893.
FT FTID=VSP_004893.
SQ SEQUENCE 591 AA; 64071 MW; 04C2A5CDB06427D5 CRC64;
Query Match 100.0%; Score 2073; DB 1; Length 591;
Best Local Similarity 100.0%; Pred. No. 9,8e-98;
Matches 399; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
1 ASGAKLAAGRPNTYPPADTDHPSRGAQGEHVDVAPNGPSAGGLAIPOSSSSSSRRPPTRA 60
194 ASGAKLAAGRPNTYPPADTDHPSRGAQGEHVDVAPNGPSAGGLAIPOSSSSSSRRPPTRA 253

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QY 61 RGAPSPGVLAGHASEPOLAPACTPPAPAVGPPGPPSPQREPPQVSHQFRAALQVVD 120
DB 254 RGAPSPGVLAGHASEPOLAPACTPPAPAVGPPGPPSPQREPPQVSHQFRAALQVVD 313
QY 121 PGDPRSYLDNFIKIGEGSTGIVCIATVRSSGKLVAVKQMLRQQRRELLFNEVIMRDY 180
DB 314 PGDPRSYLDNFIKIGEGSTGIVCIATVRSSGKLVAVKQMLRQQRRELLFNEVIMRDY 373
QY 181 QHENVEMNTSYLVGDELNVYMERLEGALTDIVTTRNNEBOIYAVCLAVLQALSTLHA 240
DB 374 QHENVEMNTSYLVGDELNVYMERLEGALTDIVTTRNNEBOIYAVCLAVLQALSTLHA 433
QY 241 QGVYHRIKSDSILLTHDGRVKLSDFGCAQVSKVPRRSVGTPTWMAPELSRLPYG 300
DB 434 QGVYHRIKSDSILLTHDGRVKLSDFGCAQVSKVPRRSVGTPTWMAPELSRLPYG 493
QY 301 PEVDIWSLGIWVEMVDEPPYNEPPLKAMKMIKRNLPRLNVLKRVSPSLKGFLLRL 360
DB 494 PEVDIWSLGIWVEMVDEPPYNEPPLKAMKMIKRNLPRLNVLKRVSPSLKGFLLRL 553
QY 361 VRDPAQATTAELKHPPLAKAGPPASIVPLMKQNRTR 398
DB 554 VRDPAQATTAELKHPPLAKAGPPASIVPLMKQNRTR 591
RESULT 2
ID Q8K0U2 PRELIMINARY; PRT; 407 AA.
AC Q8K0U2;
DT 01-OCT-2002 (TREMBLrel, 22, Created)
DT 01-OCT-2002 (TREMBLrel, 22, Last sequence update)
DT 01-MAR-2004 (TREMBLrel, 26, Last annotation update)
DE PAK4 protein (Fragment).
GN Name=PAK4;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RS SEQUENCE FROM N.A.
RC TISSUE=Eye;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Deris J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Sherman C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.T., Wang J., Heien F.,
RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udell T.B., Tothiyuki S., Carninci P., Muliyil S.J.,
RA Raha S.S., Loguclano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bozak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Huiyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Buttefield Y.S.,
RA Krzywinski M.I., Skala U., Smalins D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RS SEQUENCE FROM N.A.
RC TISSUE=Eye;
RA Strausberg R.;
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC030389; AAH030389.1; -
DR HSSP; Q13153; 1F3M.
DR MGD; MGI:1917834; PAK4.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 17, 2005, 10:00:02 ; Search time 21.3266 Seconds
(without alignments)
1795.441 Million cell updates/sec

Title: US-10-725-121A-30

Perfect score: 2073

Sequence: 1 ASGAKLAAAGPFTYTRADT.....LAKAGPASTIVPLMRQKTR 398

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|---------|---------------------|
| 1 | 911.5 | 44.0 | 540 | T19956 | hypothetical prote |
| 2 | 911.5 | 44.0 | 542 | T19952 | hypothetical prote |
| 3 | 833.5 | 40.2 | 525 | S58682 | protein kinase, p2 |
| 4 | 832.5 | 40.2 | 544 | A57597 | beta-p21-activated |
| 5 | 817.5 | 39.4 | 545 | G01773 | p21-activated prot |
| 6 | 816 | 39.4 | 544 | S40482 | serine/threonine-s |
| 7 | 815.5 | 39.3 | 544 | T49376 | p21 activated kina |
| 8 | 792 | 38.2 | 939 | S28394 | probable serine/th |
| 9 | 763.5 | 36.8 | 658 | T39500 | serine/threonine-s |
| 10 | 759 | 36.6 | 1230 | T18256 | probable serine/th |
| 11 | 759 | 36.6 | 1230 | T18259 | serine/threonine p |
| 12 | 754.5 | 36.4 | 658 | S60170 | protein kinase pak |
| 13 | 742.5 | 35.8 | 622 | T15467 | hypothetical prote |
| 14 | 722 | 34.8 | 378 | T26684 | hypothetical prote |
| 15 | 672.5 | 32.4 | 842 | S60402 | protein kinase CLA |
| 16 | 670 | 32.3 | 589 | T38086 | serine/threonine-p |
| 17 | 607.5 | 29.3 | 655 | S51884 | probable protein k |
| 18 | 498 | 24.0 | 471 | T39232 | probable serine th |
| 19 | 494 | 23.8 | 1102 | TJ06316 | probable protein k |
| 20 | 484 | 23.3 | 836 | B96716 | probable serine/th |
| 21 | 478 | 23.0 | 653 | T34356 | hypothetical prote |
| 22 | 476 | 23.0 | 819 | A53714 | protein kinase (BC |
| 23 | 470.5 | 22.7 | 839 | T29372 | hypothetical prote |
| 24 | 464 | 22.4 | 426 | S71886 | Ste20-like protein |
| 25 | 463 | 22.3 | 1231 | T18532 | serine/threonine pr |
| 26 | 462 | 22.3 | 1233 | T14157 | protein kinase SK2 |
| 27 | 460 | 22.2 | 1206 | T34021 | protein kinase SK2 |
| 28 | 458.5 | 22.1 | 690 | C96572 | protein p12M16.4 l |
| 29 | 455.5 | 22.0 | 1080 | S48944 | hypothetical prote |

| | | | | | | |
|----|-------|------|------|---|--------|--------------------|
| 30 | 455 | 21.9 | 1233 | 2 | T30989 | serine/threonine p |
| 31 | 450.5 | 21.7 | 312 | 2 | T38525 | serine/threonine p |
| 32 | 445 | 21.5 | 1001 | 2 | T17365 | serine/threonine p |
| 33 | 440.5 | 21.2 | 1075 | 2 | T27623 | hypothetical prote |
| 34 | 440.5 | 21.2 | 1080 | 2 | T27622 | hypothetical prote |
| 35 | 437.5 | 21.1 | 1062 | 2 | S46367 | protein kinase CDC |
| 36 | 428 | 20.6 | 1228 | 2 | T18897 | hypothetical prote |
| 37 | 421 | 20.3 | 553 | 2 | T01479 | hypothetical prote |
| 38 | 413 | 19.9 | 561 | 2 | T51417 | protein kinase-lik |
| 39 | 410 | 19.8 | 659 | 1 | A39723 | protein kinase byr |
| 40 | 410 | 19.8 | 883 | 2 | A96662 | hypothetical prote |
| 41 | 409.5 | 19.8 | 652 | 2 | T39722 | serine/threonine p |
| 42 | 408.5 | 19.7 | 891 | 2 | T40503 | protein kinase kin |
| 43 | 404.5 | 19.5 | 1135 | 1 | A29813 | 132k niaC protein |
| 44 | 404.5 | 19.5 | 1501 | 1 | B29813 | 174k niaC protein |
| 45 | 399.5 | 19.3 | 891 | 2 | A38903 | protein kinase 1 - |

ALIGNMENTS

| | | | | | | | | | |
|--|-----|--|-----|--|--|--|--|--|--|
| RESULT 1 | | | | | | | | | |
| T19956 hypothetical protein C45B11.1b - Caenorhabditis elegans | | | | | | | | | |
| C:Species: Caenorhabditis elegans | | | | | | | | | |
| C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 16-Aug-2004 | | | | | | | | | |
| C:Accession: T19956 | | | | | | | | | |
| R:McMurray, A. | | | | | | | | | |
| submitted to the EMBL Data Library, June 1996 | | | | | | | | | |
| A:Reference number: Z19202 | | | | | | | | | |
| A:Accession: T19956 | | | | | | | | | |
| A:Status: preliminary; translated from GB/EMBL/DBJ | | | | | | | | | |
| A:Molecule type: DNA | | | | | | | | | |
| A:Residues: 1-540 <MIL> | | | | | | | | | |
| A:Cross-references: UNIPROT:Q9U3M1; EMBL:Z74029; PIDN:CAA98433.1; GSPDB:GN00023; CESP:C4 | | | | | | | | | |
| A:Experimental source: clone C45B11 | | | | | | | | | |
| C:Genetic81 | | | | | | | | | |
| A:Gene: CESP:C45B11.1b | | | | | | | | | |
| A:Map position: 5 | | | | | | | | | |
| A:Intons: 13/2; 62/3; 104/2; 231/3; 367/2; 468/3 | | | | | | | | | |
| C:Superfamily: protein kinase homology | | | | | | | | | |
| Query Match | | | | | | | | | |
| Best Local Similarity 44.0%; Score 911.5; DB 2; Length 540; | | | | | | | | | |
| Matches 202; Conservative 48; Mismatches 104; Indels 53; Gaps 6; | | | | | | | | | |
| Qy | 31 | PHDVAPGPAAGLAIPSSSSSR-----PPTRARG-----APSP----- | 66 | | | | | | |
| Db | 119 | PSVARSLSLRISATASVNVSSARHSFRPTLPVSGRGTPRNDPSAIPPLRNQKPMs | 178 | | | | | | |
| Qy | 67 | ---GVLAGPH-----ASBPQLAPACTPAAPAVGPPGPRSPQRRP---ORVS | 107 | | | | | | |
| Db | 179 | TTTGVEKEPHQYQOIIITIVASRTTTPQLQPKS-----PSTPQAMQGPCTGVS | 228 | | | | | | |
| Qy | 108 | HEQFRALQLVNDPGDPRSTLDNFIKIGEGSTGIVCIATYRSSGKLVAVKMDIKQQR | 167 | | | | | | |
| Db | 229 | DEEFRRALKFVVNDGTDRSDLTIDYKQIGEGSTGVEAAVYISKQIVAAVVRMLRKQQR | 288 | | | | | | |
| Qy | 168 | ELLFNEVIMRDYQHEHNVEMTNSYLVGDELVMVMELEGALTDIYTHRRANBEQAAV | 227 | | | | | | |
| Db | 289 | ELLFNEVSIIRKQYOHFNIVAFSSHLVDDLMVMEEMEGSLTDIYTAIRMTBPQATI | 348 | | | | | | |
| Qy | 228 | CLAVLQALSVLAQGVIRHDIKSDIILLTHDGVKLSDFGCAQVNSKEVRRKSLVTPY | 287 | | | | | | |
| Db | 349 | SRQVLGALDFLHARKVYHRDIKSDIILKKDGVTKLTDFFGCOQLSEVFRRSLSVTPY | 408 | | | | | | |
| Qy | 288 | WMAPELISRLPYGPBVDIWSLGMVTEMVDGEPPEYFNEPPLKAMKMTKRLDPLRLKTLHK | 347 | | | | | | |
| Db | 409 | WTAAEVYIAREPYTRADIVSFGIMLIEMVGEPPFPNDQFQMKRIKRDHEARFSRHAK | 468 | | | | | | |
| Qy | 348 | VSSSLKGFDLRLVLRDPAQRATAAELKHPFLKAGGPASIVPLMRQ 394 | | | | | | | |
| Db | 469 | VSVLELSLSHCIVKQVKNKMPAKDILRHFPKAKQHSSTIAILLQ 515 | | | | | | | |

RESULT 2

T19952

hypothetical protein C45B11.1a - *Caenorhabditis elegans*C/Species: *Caenorhabditis elegans*

C/Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 16-Aug-2004

C/Accession: T19952

R/McMurray, A.

Submitted to the EMBL Data Library, June 1996

A/Reference number: Z19202

A/Accession: T19952

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1542 <M1>

A/Cross-references: UNIPROT:Q18637; EMBL:Z74029; FIDN:CAA98429.1; GSPDB:GN00023; CESP:C4

A/Experimental source: Clone C45B11

C/Genetic:

A/Map position: 5

A/Insertions: 13/2; 62/3; 104/2; 233/3; 369/2; 470/3

C/Superfamily: protein kinase homology

Query Match 44.0%; Score 911.5; DB 2; Length 542;

Best Local Similarity 49.6%; Pred. No. 1.8e-29;

Matches 202; Conservative 46; Mismatches 104; Indels 53; Gaps 6;

QY 31 PHDVAPNGPAGGAIATQSSSSSR-----PPTRRAG-----APSP----- 66
DB 121 PSVARSNSLRISATVSPVNVNSARHSFRPTLPVSGRGYPFNDPSYAPLRLNQKPPMS 180

QY 67 ---GVLAGPH-----ASEPOLAPACTPAAPAVNGPPRSPORP---ORVS 107
DB 181 TTREVEKPHQYQOITTVAPSRITTPQLOPKS-----PSTPQAKRQPKCTEGVS 230

QY 108 HEQFRALQLVNDVDBPRSYLDNFIKIGEGSTGVICIAVTVSSGKLVAVKMDLRKQOR 167
DB 231 DEERNAKLKFFVNDGTDRSDLTQKQIGEGSTGVVAAYKISTQIVAVKMDLRKQOR 290

QY 168 ELFENEVIMADYHENVNENKSYLVGDELMVMEPLLEGALTDIYTHMEEQIAAV 227
DB 291 ELTFENEVSILRQYHPPIVRFSSHLVDDELVMVMEFEGSLTDIYVATMTPEQIATI 350

QY 228 CLATQALSYLAAGVHRDVKSDSILLTHDGRVYKLSDFGCAOVSKVPRKSLVGTPT 287
DB 351 SRQVLGALDPLHAKVHRDKSDSILLKRDGYKLTDFGCGQLSEVPRRSLVGTPT 410

QY 288 WMABELISRLPYGPEVDIWSLGIWIEVNDGEPPEYFNEPPLKAMKIRDNLPPLKMLHK 347
DB 411 WTAEEVIAREPYDRADIMSGIMLIEVGEPPFPFNDQFQAKKRIRIDEHEAFSRHAK 470

QY 348 VSPSLKGFRLRLVDRPAQRATAABELKHPPLAKAGPPASIVPLMRQ 394
DB 471 VSVLSLSLSHCIVDKVWKPKADLRLHPPFAKAQSSSIAPLLQ 517

RESULT 3

S58682

protein kinase, p21-activated (EC 2.7.1.-) - human

N/Alternate names: protein kinase PAK65; S6/H4 kinase

C/Species: *Homo sapiens* (man)

C/Date: 22-Aug-1996 #sequence_revision 06-Sep-1996 #text_change 16-Aug-2004

C/Accession: S58682; S55304; S58690; A57441

R/Sellier, M.; Krause, U.U.; Bagrodia, S.; Ambrose, D.; Bokoch, G.M.; Chernoff, J.

Submitted to the EMBL Data Library, April 1995

A/Description: Human p21-activated protein kinases regulate actin organization in mamma

A/Reference number: S58682

A/Accession: S58682

A/Molecule type: DNA

A/Residues: 1525 <SEL>

A/Cross-references: UNIPROT:Q13177; EMBL:U24153; NID:9780807; PIDN:AAA65442.1; PID:97808

R/Martin, G.A.; Bollag, G.; McCormick, F.; Abo, A.

EMBO J. 14, 1970-1978, 1995

A/Title: A novel serine kinase activated by rac1/CDCA2Hs-dependent autophosphorylation
A/Reference number: S55258; MUID:95262637; PMID:7744004
A/Accession: S55258

A/Status: not compared with conceptual translation

A/Molecule type: mRNA

A/Residues: 1525

A/Accession: S55304

A/Molecule type: protein

A/Residues: 402-418 <MAW>

R/Martin, G.A.; Bollag, G.; McCormick, F.; Abo, A.

EMBO J. 14, 4385, 1995

A/Reference number: S58690; MUID:96016211; PMID:7556080

A/Contents: erratum

A/Accession: S58690

A/Status: not compared with conceptual translation

A/Molecule type: mRNA

A/Residues: 1-30 <MAP>

R/Banner, G.E.; Dennis, P.B.; Maesacchia, R.A.

J. Biol. Chem. 270, 21121-21128, 1995

A/Title: Activation of an S6/H4 kinase (PAK 65) from human placenta by intramolecular and

A/Reference number: A57441; MUID:95403344; PMID:7673144

A/Accession: A57441

A/Molecule type: protein

A/Residues: 197-216;402,'S',404-409 <BEN>

A/Experimental source: placenta

C/Superfamily: protein kinase homology

C/Keywords: ATP; autophosphorylation; phosphoprotein; phosphotransferase; serine/threonine

F/247-501/domain; protein kinase homology <KIN>

F/255-263/Region; protein kinase ATP-binding motif

F/197,402/Binding site: phosphate (Ser) (covalent) #status predicted

Query Match 40.2%; Score 833.5; DB 2; Length 525;
Best Local Similarity 44.6%; Pred. No. 2e-26;
Matches 173; Conservative 69; Mismatches 109; Indels 37; Gaps 6;

QY 39 PSAGGAIIPSSSSSRPPTRRAGAPSGVLAGPHA-SEPOLAPACTP----- 85
DB 145 PEKQGL-----PSGTPALNAKTEAPAVTTEEDDEETAPVLAIPRDHTSIYTRS 197

QY 86 AARAVPPPPPPR-----SPQREQRVSHQFRALQLVNDPQPRSYLDNFIIGE 136
DB 198 VIDPVPAPVDSHVDGAKSLDKQKPKMTDEIRKELTIYSIGPKKRYRYEYIGQ 257

QY 137 GSTGIVCIATVRSRSGKLVAAKMDLRKQORELTFNEVIMRDYHENVEMTVSYLVD 196
DB 258 GASGTVFAIDVALGCVALKQINLQKPKKELINELIMKELKNINYPFDSYLVGD 317

QY 197 ELWVMEFLGALTDIVTHTR-MNEEQIAVCLAVLQALSVLAQGVHRDIKSDSILL 255
DB 318 ELFVMEYLAGSLTDVVTETACWDEAQIAVCRECLQALEFLHANGVHRDIKSDVLL 377

QY 256 THDGRVYLSDFGCAOVSKVPRKSLVGTPTMMAPBLISRLPYGPEVDIWSLGIWIE 315
DB 378 GMEGSVLTDFGFAQITTPQSSKSTVGGTPYMMAPVPRKAVGPRVDIWSLGIWIE 437

QY 316 VDGEPPYENEPPLKAMKIRDNLPPLKMLHKVSPSLKGFRLRLVNDPQPRATAELIK 375
DB 438 VEGEPYTLNENPLRALVILATNGPBLQNPBKLSPIRDLINCLMDVKEKSGAKELIQ 497

QY 376 HPFLAKAGPPASIVPL-----MRQNR 396
DB 498 HPFLAKLAPSLSLPLIMAKKAKSNR 525

RESULT 4

A57597

beta-p21-activated protein kinase - rat

N/Alternate names: beta-PAK

C/Species: *Rattus norvegicus* (Norway rat)

C/Date: 08-Feb-1996 #sequence_revision 08-Feb-1996 #text_change 09-Jul-2004

C/Accession: A57597

R/Manser, E.; Chong, C.; Zhao, Z.S.; Leung, T.; Michael, G.; Hall, C.; Lim, L.

J. Biol. Chem. 270, 25070-25078, 1995

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 17, 2005, 09:50:45 ; Search time 94.1678 Seconds

(Without alignments)
1634.641 Million cell updates/sec

Title: US-10-725-121A-30

Perfect score: 2073

Sequence: 1 ASGAKLAAGPFTYPRADR.....LAKGPPASIVPLMRQNR 398

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_16Dec04:*
1: geneseqp1980s:*
2: geneseqp1980s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|--------------------|
| 1 | 2073 | 100.0 | 398 | 2 | AAV55941 Human PAK |
| 2 | 2073 | 100.0 | 591 | 2 | AAV55964 Full leng |
| 3 | 2073 | 100.0 | 591 | 3 | AAV59128 Human ser |
| 4 | 2073 | 100.0 | 591 | 7 | ADG37307 Nuclear f |
| 5 | 2073 | 100.0 | 591 | 7 | ADG89973 Human can |
| 6 | 2073 | 100.0 | 591 | 7 | ADG45079 Human kin |
| 7 | 2073 | 100.0 | 591 | 8 | ADH23362 Human p21 |
| 8 | 2073 | 100.0 | 591 | 8 | ABM82101 |
| 9 | 2073 | 100.0 | 620 | 4 | ABG19308 |
| 10 | 2069 | 99.8 | 522 | 8 | ABM84642 Human dia |
| 11 | 2069 | 99.8 | 522 | 8 | ABM84644 Human dia |
| 12 | 2069 | 99.8 | 522 | 8 | ABM84645 Human dia |
| 13 | 2058 | 99.3 | 588 | 8 | ADH23359 Human p21 |
| 14 | 1963 | 94.7 | 593 | 8 | ADJ96654 Human p21 |
| 15 | 1926 | 92.9 | 501 | 7 | ADG37309 Nuclear f |
| 16 | 1925 | 92.9 | 438 | 7 | ADG37305 Nuclear f |
| 17 | 1917 | 92.5 | 438 | 8 | ADG3763 Human kin |
| 18 | 1645 | 79.4 | 517 | 8 | ABM84648 Human dia |
| 19 | 1645 | 79.4 | 517 | 8 | ABM84647 Human dia |
| 20 | 1645 | 79.4 | 517 | 8 | ABM84643 Human dia |
| 21 | 1645 | 79.4 | 517 | 8 | ABM84646 Human dia |
| 22 | 1502 | 72.5 | 293 | 7 | ADG15851 PAK4XD pr |
| 23 | 1351 | 65.2 | 719 | 7 | ADJ83007 Murine ma |
| 24 | 1345 | 64.9 | 719 | 4 | AAV38963 Human pol |
| 25 | 1340 | 64.6 | 719 | 4 | AAV55705 Novel pro |

| | | | | | | |
|----|--------|------|-----|---|----------|--------------------|
| 26 | 1340 | 64.6 | 719 | 7 | ADG37451 | ADG37451 Nuclear f |
| 27 | 1340 | 64.6 | 719 | 7 | ADP45080 | ADP45080 Human kin |
| 28 | 1340 | 64.6 | 719 | 7 | ADJ83008 | ADJ83008 Human mam |
| 29 | 1340 | 64.6 | 719 | 8 | ADJ29314 | ADJ29314 Human MAR |
| 30 | 1339 | 64.6 | 719 | 4 | AAE02187 | AAE02187 Human p21 |
| 31 | 1330 | 64.2 | 457 | 8 | ADH42207 | ADH42207 Novel hum |
| 32 | 1330 | 64.2 | 457 | 8 | ADH42215 | ADH42215 Novel hum |
| 33 | 1330 | 64.2 | 457 | 8 | ADH42211 | ADH42211 Novel hum |
| 34 | 1330 | 64.2 | 457 | 8 | ADH42217 | ADH42217 Novel hum |
| 35 | 1330 | 64.2 | 457 | 8 | ADH42213 | ADH42213 Novel hum |
| 36 | 1277 | 61.6 | 250 | 3 | AAV59129 | AAV59129 Human PAK |
| 37 | 1255.5 | 60.6 | 639 | 8 | ADH23364 | ADH23364 Fruit fly |
| 38 | 1252.5 | 60.4 | 635 | 8 | ADH23360 | ADH23360 Fruit fly |
| 39 | 1241 | 59.9 | 240 | 4 | AAV93297 | AAV93297 Human pol |
| 40 | 1241 | 59.9 | 240 | 7 | ADG37303 | ADG37303 Nuclear f |
| 41 | 1241 | 59.9 | 240 | 8 | ADL30760 | ADL30760 Human pro |
| 42 | 1205 | 58.1 | 338 | 7 | ADL22704 | ADL22704 Human dis |
| 43 | 1205 | 58.1 | 547 | 4 | AAV67825 | AAV67825 Human p21 |
| 44 | 1197 | 57.7 | 681 | 2 | AAV55940 | AAV55940 Human PAK |
| 45 | 1197 | 57.7 | 681 | 3 | AAV03967 | AAV03967 Signal tr |

ALIGNMENTS

| | |
|----------|--|
| RESULT 1 | AAV55941 standard; protein; 398 AA. |
| ID | AAV55941 |
| XX | AAV55941; |
| AC | 18-FEB-2000 (first entry) |
| DT | Human PAK5 protein. |
| XX | |
| XX | Antithrombotic; antithrombotic; antiinflammatory; antiallergic; osteopathic; |
| KW | antiproliferative; antiarteriosclerotic; antisthmatic; immunosuppressive; |
| KW | neuroprotective; cardiact; cerebroprotective; cytoskeletal; antidiabetic; |
| KW | vulner; STS20; protein kinase; STK2; STK3; STK4; STK5; STK6; STK7; |
| KW | ZC1; ZC2; ZC3; ZC4; KHS2; STU1; STU3; STU4; STU5; PAK4; PAK5; antagonist; |
| KW | antibody; gene therapy; rheumatoid arthritis; arteriosclerosis; asthma; |
| KW | inflammatory bowel disease; Crohn's disease; osteoarthritis; psoriasis; |
| KW | rhinitis; autoimmunity; organ transplantation; multiple sclerosis; |
| KW | myocardial infarction; cardiovascular disease; stroke; renal failure; |
| KW | oxidative stress-related neurodegenerative disorder; Parkinson's disease; |
| KW | amyotrophic lateral sclerosis; Leigh syndrome; cancer; cardiomyopathy; |
| KW | ischemic disorder; inflammation; diabetes mellitus; fibrosis; microsis; |
| KW | mesangial disorder; growth regulation; wound healing; T cell activation; |
| KW | immunosuppressant. |
| XX | |
| OS | Homo sapiens. |
| XX | |
| PN | MO9953036-AA2. |
| XX | |
| PD | 21-OCT-1999. |
| XX | |
| PF | 13-APR-1999; 99MO-US008150. |
| XX | |
| PR | 14-APR-1998; 98US-0081784P. |
| XX | |
| PA | (SUGR-) SUGEN INC. |
| XX | |
| PI | Plowman G, Martinez R, Whyte D; |
| XX | |
| DR | WPI; 1999-611301/52. |
| XX | |
| DR | N-PADB; AA240493. |
| XX | |
| PT | Novel kinase-related polypeptides used for the diagnosis and treatment of |
| XX | kinase-related diseases and disorders. |
| PS | Disclosure; Page 310-312; 387pp; English. |
| XX | |
| CC | This sequence represents a novel STB20-related protein kinase. The |

CC invention relates to nucleic acid molecule encoding a kinase polypeptide
 CC selected from STK1, STK2, STK3, STK4, STK5, STK6, STK7, ZC1, ZC2, ZC3,
 CC ZC4, KHS2, SULU1, SULU3, GSK2, PAK4 and PAK5. The proteins are used to
 CC identify agonists and antagonists, and to raise antibodies. The
 CC polynucleotides are useful in gene therapy protocols. The polynucleotides,
 CC polypeptides, antibodies, antagonists and agonists may be used to treat
 CC diseases such as immune-related disorders and diseases (e.g., rheumatoid
 CC arthritis, atherosclerosis, chronic inflammatory bowel disease (e.g.,
 CC Crohn's disease), asthma, osteoarthritis, psoriasis, atherosclerosis,
 CC rhinitis, autoimmunity, and organ transplantation, chronic inflammatory
 CC pelvic disease, multiple sclerosis, organ transplantation, myocardial
 CC infarction, cardiovascular disease, stroke, renal failure, oxidative
 CC stress-related neurodegenerative disorders (e.g., amyotrophic lateral
 CC sclerosis, Parkinson's disease and Leigh syndrome), cancer,
 CC cardiomyopathies, ischemic disorders, inflammatory disorders, diabetes
 CC mellitus, fibrotic and mesangial disorders. The proteins may also be
 CC useful for cell growth regulation (e.g. in wound healing), T cell
 CC activation, mitosis control, and as immunosuppressants

XX Sequence 398 AA:

Query Match 100.0%; Score 2073; DB 2; Length 398;
 Best Local Similarity 100.0%; Pred. No. 1.9e-157;
 Matches 398; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 DB 1 ASGAKLAAGRPNTYPRADTDHPSRGAQGEPHDVAHPNGPSAGLAIPQSSSSSRPPTRA 60
 QY 61 RGAPSPGVLPNASEPOLAPACTPAAPAVGPPGPPSPQREPPRVSHQRFALQLVVD 120
 DB 61 RGAPSPGVLPNASEPOLAPACTPAAPAVGPPGPPSPQREPPRVSHQRFALQLVVD 120
 QY 121 PGDPSTYLDNPKIKGEGSTGIVCIATVRSSGKLVAVKMDLRKQRRRELLFNEVVIKRDY 180
 DB 121 PGDPSTYLDNPKIKGEGSTGIVCIATVRSSGKLVAVKMDLRKQRRRELLFNEVVIKRDY 180
 QY 181 QHEVNVEMNYSYLVGDELMVMEFLBEGALTDIYTHRNMEQJIAVCLAVLQALSVLHA 240
 DB 181 QHEVNVEMNYSYLVGDELMVMEFLBEGALTDIYTHRNMEQJIAVCLAVLQALSVLHA 240
 QY 241 QGVHHRDKSDSILLTHDGRVKLSDFGCAQVSKVPRRSKLVGTPTWMADELISRLPYG 300
 DB 241 QGVHHRDKSDSILLTHDGRVKLSDFGCAQVSKVPRRSKLVGTPTWMADELISRLPYG 300
 QY 301 PEVDIWSLGIWLEMDVGBEPYFNEPPLKAMKMRDNLPRLLKYLHKVSPSLKGFDRLL 360
 DB 301 PEVDIWSLGIWLEMDVGBEPYFNEPPLKAMKMRDNLPRLLKYLHKVSPSLKGFDRLL 360
 QY 361 VRDPAQRATAELKHPFLAKAGPPASIVPLMRQRRR 398
 DB 361 VRDPAQRATAELKHPFLAKAGPPASIVPLMRQRRR 398

RESULT 2

AAVS5964
 ID AAVS5964 standard; protein; 591 AA.

XX AAVS5964,
 DT 18-FEB-2000 (first entry)
 XX

DE Full length human PAK5 protein.

XX Antirheumatic; antiarthritic; antiinflammatory; antiallergic; osteopathic;
 KW antiporiatic; antiarteriosclerotic; antiasthmatic; immunosuppressive;
 KW neuroprotective; cardiatic; cerebroprotective; cytoskeletal; antidiabetic;
 KW vulnery; STB20; protein kinase; STK2; STK3; STK4; STK5; STK6; STK7;
 KW ZC1; ZC2; ZC3; KHS2; SULU1, SULU3, GSK2, PAK4, PAK5, antagonist;
 KW antibody; gene therapy; rheumatoid arthritis; atherosclerosis; asthma;
 KW inflammatory bowel disease; Crohn's disease; osteoarthritis; psoriasis;
 KW rhinitis; autoimmunity; organ transplantation; multiple sclerosis;
 KW myocardial infarction; cardiovascular disease; stroke; renal failure;

KM oxidative stress-related neurodegenerative disorder; Parkinson's disease;
 KW amyotrophic lateral sclerosis; leigh syndrome; cancer; cardiomyopathy;
 KW ischemic disorder; inflammation; diabetes mellitus; fibrosis; mitosis;
 KW mesangial disorder; growth regulation; wound healing; T cell activation;
 KW immunosuppressant.

XX Homo sapiens.
 XX PN M09953036-A2.
 XX PD 21-OCT-1999.

XX 13-APR-1999; 99MO-US008150.
 XX 14-APR-1998; 98US-0081784P.

XX (SUGB-) SUGEN INC.
 XX PI Plowman G, Martinez R, Whyte D,
 XX PI WPI; 1999-611301/52.

XX DR N-PSDB; AA240538.
 XX PT Novel kinase-related polypeptides used for the diagnosis and treatment of
 XX PT kinase-related diseases and disorders.

XX Claim 11; Page 366-368; 387pp; English.

XX This sequence represents a novel STK2-related protein kinase. The
 CC invention relates to nucleic acid molecule encoding a kinase polypeptide
 CC selected from STK1, STK2, STK3, STK4, STK5, STK6, STK7, ZC1, ZC2, ZC3,
 CC ZC4, KHS2, SULU1, SULU3, GSK2, PAK4 and PAK5. The proteins are used to
 CC identify agonists and antagonists, and to raise antibodies. The
 CC polynucleotides are useful in gene therapy protocols. The polynucleotides,
 CC polypeptides, antibodies, antagonists and agonists may be used to treat
 CC diseases such as immune-related disorders and diseases (e.g., rheumatoid
 CC arthritis, atherosclerosis, chronic inflammatory bowel disease (e.g.,
 CC Crohn's disease), asthma, osteoarthritis, psoriasis, atherosclerosis,
 CC rhinitis, autoimmunity, and organ transplantation, chronic inflammatory
 CC pelvic disease, multiple sclerosis, organ transplantation, myocardial
 CC infarction, cardiovascular disease, stroke, renal failure, oxidative
 CC stress-related neurodegenerative disorders (e.g., amyotrophic lateral
 CC sclerosis, Parkinson's disease and Leigh syndrome), cancer,
 CC cardiomyopathies, ischemic disorders, inflammatory disorders, diabetes
 CC mellitus, fibrotic and mesangial disorders. The proteins may also be
 CC useful for cell growth regulation (e.g. in wound healing), T cell
 CC activation, mitosis control, and as immunosuppressants

XX Sequence 591 AA:

Query Match 100.0%; Score 2073; DB 2; Length 591;
 Best Local Similarity 100.0%; Pred. No. 3.2e-157;
 Matches 398; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ASGAKLAAGRPNTYPRADTDHPSRGAQGEPHDVAHPNGPSAGLAIPQSSSSSRPPTRA 60
 DB 194 ASGAKLAAGRPNTYPRADTDHPSRGAQGEPHDVAHPNGPSAGLAIPQSSSSSRPPTRA 253
 QY 61 RGAPSPGVLPNASEPOLAPACTPAAPAVGPPGPPSPQREPPRVSHQRFALQLVVD 120
 DB 254 RGAPSPGVLPNASEPOLAPACTPAAPAVGPPGPPSPQREPPRVSHQRFALQLVVD 313
 QY 121 PGDPSTYLDNPKIKGEGSTGIVCIATVRSSGKLVAVKMDLRKQRRRELLFNEVVIKRDY 180
 DB 314 PGDPSTYLDNPKIKGEGSTGIVCIATVRSSGKLVAVKMDLRKQRRRELLFNEVVIKRDY 373
 QY 181 QHEVNVEMNYSYLVGDELMVMEFLBEGALTDIYTHRNMEQJIAVCLAVLQALSVLHA 240
 DB 374 QHEVNVEMNYSYLVGDELMVMEFLBEGALTDIYTHRNMEQJIAVCLAVLQALSVLHA 433
 QY 241 QGVHHRDKSDSILLTHDGRVKLSDFGCAQVSKVPRRSKLVGTPTWMADELISRLPYG 300
 DB 434 QGVHHRDKSDSILLTHDGRVKLSDFGCAQVSKVPRRSKLVGTPTWMADELISRLPYG 493

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 17, 2005, 10:04:33 ; Search time 57.9494 Seconds
(without alignments)
2873.660 Million cell updates/sec

Title: US-10-725-121A-30

Perfect score: 2073
Sequence: 1 ASGAKLAAGRPNTYPRADT.....LAKAGPPASIVPLMRQNRTR 398

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867879 seqs, 418409474 residues

Total number of hits satisfying chosen parameters: 1867879

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA:*
1: /cgn2_6/ptodata/1/pubppaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/1/pubppaa/PCT_NEW_PUB.pep:*
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22: /cgn2_6/ptodata/1/pubppaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length DB | ID | Description |
|------------|-------|-------------|-----------|----|--|
| 1 | 2073 | 100.0 | 398 | 10 | US-09-291-417-30 Sequence 30, Appl |
| 2 | 2073 | 100.0 | 398 | 16 | US-10-725-329-30 Sequence 30, Appl |
| 3 | 2073 | 100.0 | 398 | 18 | US-10-725-121-30 Sequence 103, App |
| 4 | 2073 | 100.0 | 591 | 10 | US-09-291-417-103 Sequence 4, Appl |
| 5 | 2073 | 100.0 | 591 | 14 | US-10-134-102-4 Sequence 4, Appl |
| 6 | 2073 | 100.0 | 591 | 15 | US-10-394-322A-48 Sequence 2, Appl |
| 7 | 2073 | 100.0 | 591 | 15 | US-10-693-367-2 Sequence 4, Appl |
| 8 | 2073 | 100.0 | 591 | 16 | US-10-725-329-103 Sequence 103, App |
| 9 | 2073 | 100.0 | 591 | 17 | US-10-693-025-5 Sequence 5, Appl |
| 10 | 2073 | 100.0 | 591 | 18 | US-10-725-121-103 Sequence 103, App |
| 11 | 2073 | 100.0 | 591 | 18 | US-10-509-599-18 Sequence 18, Appl |

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|----|--------|-------|-----|----|--|
| 12 | 2073 | 100.0 | 620 | 18 | US-10-450-763-49667 Sequence 49667, A |
| 13 | 2058 | 99.3 | 588 | 14 | US-10-134-102-1 Sequence 1, Appl |
| 14 | 1963 | 94.7 | 593 | 16 | US-10-618-941-111 Sequence 11, App |
| 15 | 1502 | 72.5 | 292 | 15 | US-10-406-676-5 Sequence 5, Appl |
| 16 | 1502 | 72.5 | 292 | 15 | US-10-406-676-6 Sequence 6, Appl |
| 17 | 1502 | 72.5 | 292 | 15 | US-10-406-676-8 Sequence 8, Appl |
| 18 | 1502 | 72.5 | 292 | 15 | US-10-406-676-9 Sequence 9, Appl |
| 19 | 1502 | 72.5 | 292 | 15 | US-10-406-676-10 Sequence 10, Appl |
| 20 | 1502 | 72.5 | 292 | 15 | US-10-406-676-11 Sequence 11, Appl |
| 21 | 1502 | 72.5 | 293 | 15 | US-10-406-676-4 Sequence 4, Appl |
| 22 | 1481 | 71.4 | 292 | 15 | US-10-406-676-7 Sequence 7, Appl |
| 23 | 1481 | 71.4 | 292 | 15 | US-10-406-676-12 Sequence 12, Appl |
| 24 | 1421 | 68.5 | 292 | 15 | US-10-406-676-15 Sequence 15, Appl |
| 25 | 1351 | 65.2 | 719 | 14 | US-10-331-095-2 Sequence 2, Appl |
| 26 | 1340 | 64.6 | 719 | 14 | US-10-331-095-4 Sequence 4, Appl |
| 27 | 1340 | 64.6 | 719 | 15 | US-10-394-322A-49 Sequence 49, Appl |
| 28 | 1303 | 62.9 | 290 | 15 | US-10-406-676-13 Sequence 13, Appl |
| 29 | 1289 | 62.2 | 290 | 15 | US-10-406-676-14 Sequence 14, Appl |
| 30 | 1289 | 62.2 | 290 | 15 | US-10-406-676-16 Sequence 16, Appl |
| 31 | 1289 | 62.2 | 290 | 15 | US-10-406-676-17 Sequence 17, Appl |
| 32 | 1277 | 61.6 | 250 | 15 | US-10-693-367-3 Sequence 3, Appl |
| 33 | 1255.5 | 60.6 | 639 | 14 | US-10-134-102-6 Sequence 6, Appl |
| 34 | 1252.5 | 60.4 | 635 | 14 | US-10-134-102-2 Sequence 2, Appl |
| 35 | 1213 | 58.5 | 290 | 15 | US-10-406-676-18 Sequence 18, Appl |
| 36 | 1209 | 58.3 | 290 | 15 | US-10-406-676-19 Sequence 19, Appl |
| 37 | 1209 | 58.3 | 290 | 15 | US-10-406-676-20 Sequence 20, Appl |
| 38 | 1197 | 57.7 | 681 | 10 | US-09-291-417-29 Sequence 29, Appl |
| 39 | 1197 | 57.7 | 681 | 16 | US-10-725-329-29 Sequence 29, Appl |
| 40 | 1197 | 57.7 | 681 | 16 | US-10-737-450-108 Sequence 108, App |
| 41 | 1197 | 57.7 | 681 | 16 | US-10-885-921-10 Sequence 10, App |
| 42 | 1197 | 57.7 | 681 | 18 | US-10-725-121-29 Sequence 29, Appl |
| 43 | 1194 | 57.6 | 681 | 10 | US-09-765-815-2 Sequence 209, Appl |
| 44 | 1186.5 | 57.2 | 682 | 18 | US-10-840-512-209 Sequence 21, Appl |
| 45 | 1147 | 55.3 | 292 | 15 | US-10-406-676-21 Sequence 21, Appl |

ALIGNMENTS

RESULT 1
US-09-291-417-30
; Sequence 30, Application US/09291417A
; Publication No. US20030050230A1
; GENERAL INFORMATION:
; APPLICANT: PLOMMAN, GREGORY
; APPLICANT: MARTINEZ, RICARDO
; APPLICANT: MAYHE, DAVID
; TITLE OF INVENTION: STE20-RELATED PROTEIN KINASRS
; FILE REFERENCE: 240/300
; CURRENT APPLICATION NUMBER: US/09/291,417A
; CURRENT FILING DATE: 1999-04-13
; EARLIER APPLICATION NUMBER: US 60/081,784
; EARLIER FILING DATE: 1999-04-14
; NUMBER OF SEQ. ID NOS: 147
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 30
; LENGTH: 398
; TYPE: PRT
; ORGANISM: Mammalian (Human) PAK5
US-09-291-417-30

Query Match 100.0%; Score 2073; DB 10; Length 398;
Best Local Similarity 100.0%; Pred. No. 1.4e-128;
Matches 398; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ASGAKLAAGRPNTYPRADTDPHSRGAQSPHYVAPVSPAGGATPOSSSSSRPPTRA 60
DB 1 ASGAKLAAGRPNTYPRADTDPHSRGAQSPHYVAPVSPAGGATPOSSSSSRPPTRA 60
QY 61 RGAPSPGVLPSPHASEPQALAPACTPAAPVAPGCPGSPSPORSPORVSHQOFRAALQVVD 120
DB 61 RGAPSPGVLPSPHASEPQALAPACTPAAPVAPGCPGSPSPORSPORVSHQOFRAALQVVD 120

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DB 121 PGDPRSYLDNFIKIGESTGIVCIATVRSSGKLVAVKMDLRKQORRELLFNEVIMRDY 180
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DB 181 QHENVVMYNSYLVGDELMVMEFLGEGALTDIVTHTRMNEEQIAAVCLAVLQALSVLHA 240
QY 241 QGVTHRDIKSDSILTLTHDGRVKLSDFGCAQVSKEVPRRSKSLVGTPTWMABELISRLPYG 300
DB 241 QGVTHRDIKSDSILTLTHDGRVKLSDFGCAQVSKEVPRRSKSLVGTPTWMABELISRLPYG 300
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DB 361 VRDPAQRATAEELKHFFLAKAGPPASIVPLMRQNRTR 398

RESULT 2

US-10-725-329-30
; Sequence 30, Application US/10725329
; Publication No. US20040224323A1
; GENERAL INFORMATION:
; APPLICANT: PLOMMAN, GREGORY
; APPLICANT: MARTINEZ, RICARDO
; APPLICANT: WHITE, DAVID
; TITLE OF INVENTION: STE20-RELATED PROTEIN KINASES
; FILE REFERENCE: 038602/0328
; CURRENT APPLICATION NUMBER: US/10/725,329
; CURRENT FILING DATE: 2003-12-02
; PRIOR APPLICATION NUMBER: US/09/688,188B
; PRIOR FILING DATE: 2000-10-16
; PRIOR APPLICATION NUMBER: 09/291,417
; PRIOR FILING DATE: 1999-04-14
; PRIOR APPLICATION NUMBER: 60/081,784
; PRIOR FILING DATE: 1998-04-14
; NUMBER OF SEQ ID NOS: 155
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 30
; LENGTH: 398
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-725-329-30

Query Match 100.0%; Score 2073; DB 16; Length 398;

Best Local Similarity 100.0%; Pred. No. 1,4e-128;
Matches 398; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ASGAKLAAGRPFNTYPPRADTDHPSRGAQGEPRHDVAFNGPSAGGLAIPQSSSSSRPPTRA 60
DB 1 ASGAKLAAGRPFNTYPPRADTDHPSRGAQGEPRHDVAFNGPSAGGLAIPQSSSSSRPPTRA 60
QY 61 RGAPSPGVLPGBHASEPQLAPACTPAAPAVGPPGPPSPQREPORVSHQGRALQLVVD 120
DB 61 RGAPSPGVLPGBHASEPQLAPACTPAAPAVGPPGPPSPQREPORVSHQGRALQLVVD 120
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DB 121 PGDPRSYLDNFIKIGESTGIVCIATVRSSGKLVAVKMDLRKQORRELLFNEVIMRDY 180
QY 181 QHENVVMYNSYLVGDELMVMEFLGEGALTDIVTHTRMNEEQIAAVCLAVLQALSVLHA 240
DB 181 QHENVVMYNSYLVGDELMVMEFLGEGALTDIVTHTRMNEEQIAAVCLAVLQALSVLHA 240
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QY 361 VRDPAQRATAEELKHFFLAKAGPPASIVPLMRQNRTR 398
DB 361 VRDPAQRATAEELKHFFLAKAGPPASIVPLMRQNRTR 398

RESULT 3

US-10-725-121-30
; Sequence 30, Application US/10725121
; Publication No. US20050142625A1
; GENERAL INFORMATION:
; APPLICANT: PLOMMAN, GREGORY
; APPLICANT: MARTINEZ, RICARDO
; APPLICANT: WHITE, DAVID
; TITLE OF INVENTION: STE20-RELATED PROTEIN KINASES
; FILE REFERENCE: 038602/0328
; CURRENT APPLICATION NUMBER: US/10/725,121
; CURRENT FILING DATE: 2003-12-02
; PRIOR APPLICATION NUMBER: US/09/688,188B
; PRIOR FILING DATE: 2000-10-16
; PRIOR APPLICATION NUMBER: 09/291,417
; PRIOR FILING DATE: 1999-04-14
; PRIOR APPLICATION NUMBER: 60/081,784
; PRIOR FILING DATE: 1998-04-14
; NUMBER OF SEQ ID NOS: 155
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 30
; LENGTH: 398
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-725-121-30

Query Match 100.0%; Score 2073; DB 18; Length 398;
Best Local Similarity 100.0%; Pred. No. 1,4e-128;
Matches 398; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ASGAKLAAGRPFNTYPPRADTDHPSRGAQGEPRHDVAFNGPSAGGLAIPQSSSSSRPPTRA 60
DB 1 ASGAKLAAGRPFNTYPPRADTDHPSRGAQGEPRHDVAFNGPSAGGLAIPQSSSSSRPPTRA 60
QY 61 RGAPSPGVLPGBHASEPQLAPACTPAAPAVGPPGPPSPQREPORVSHQGRALQLVVD 120
DB 61 RGAPSPGVLPGBHASEPQLAPACTPAAPAVGPPGPPSPQREPORVSHQGRALQLVVD 120
QY 121 PGDPRSYLDNFIKIGESTGIVCIATVRSSGKLVAVKMDLRKQORRELLFNEVIMRDY 180
DB 121 PGDPRSYLDNFIKIGESTGIVCIATVRSSGKLVAVKMDLRKQORRELLFNEVIMRDY 180
QY 181 QHENVVMYNSYLVGDELMVMEFLGEGALTDIVTHTRMNEEQIAAVCLAVLQALSVLHA 240
DB 181 QHENVVMYNSYLVGDELMVMEFLGEGALTDIVTHTRMNEEQIAAVCLAVLQALSVLHA 240
QY 241 QGVTHRDIKSDSILTLTHDGRVKLSDFGCAQVSKEVPRRSKSLVGTPTWMABELISRLPYG 300
DB 241 QGVTHRDIKSDSILTLTHDGRVKLSDFGCAQVSKEVPRRSKSLVGTPTWMABELISRLPYG 300
QY 301 PEVDIWSLGIWVEMVDEBPPEYFNEPPLKAMKMRDNLPRLLKHLHVSPSLKGFLDRLL 360
DB 301 PEVDIWSLGIWVEMVDEBPPEYFNEPPLKAMKMRDNLPRLLKHLHVSPSLKGFLDRLL 360
QY 361 VRDPAQRATAEELKHFFLAKAGPPASIVPLMRQNRTR 398
DB 361 VRDPAQRATAEELKHFFLAKAGPPASIVPLMRQNRTR 398

RESULT 4

US-09-291-417-103
; Sequence 103, Application US/09291417A
; Publication No. US20030050230A1
; GENERAL INFORMATION:
; APPLICANT: PLOMMAN, GREGORY
; APPLICANT: MARTINEZ, RICARDO

Db 301 PEVDWISLGIWVEMVDGEPYFNEPPLKAMKMI RDNLPRLKNLHKVSPSLKGF LDRLL 360

Qy 361 VRDPAQRATAAEILKHPFLAKAGPPASIVPLMRQNRTR 398

Db 361 VRDPAQRATAAEILKHPFLAKAGPPASIVPLMRQNRTR 398

RESULT 2

US-09-291-417D-30

Sequence 30, Application US/09291417D

Patent No. 6680170

GENERAL INFORMATION:

APPLICANT: PLOMMAN, GREGORY

APPLICANT: MARTINEZ, RICARDO

APPLICANT: WHITE, DAVID

TITLE OF INVENTION: STE20-RELATED PROTEIN KINASES

FILE REFERENCE: 038602/0329

CURRENT APPLICATION NUMBER: US/09/291,417D

PRIOR FILING DATE: 1999-04-13

PRIOR FILING DATE: 1998-04-14

NUMBER OF SEQ ID NOS: 155

SOFTWARE: Patentln Ver. 2.1

SEQ ID NO 30

LENGTH: 398

TYPE: PR

ORGANISM: Homo sapiens

US-09-291-417D-30

Query Match 100.0%; Score 2073; DB 4; Length 398;
Best Local Similarity 100.0%; Pred. No. 1.8e-155;

Matches 398; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ASGAKLAAGRPNTYPPRADTDHPSRGAQGEPHDVAENGPSAGGLATPQSSSSSSRPPTRA 60

Db 1 ASGAKLAAGRPNTYPPRADTDHPSRGAQGEPHDVAENGPSAGGLATPQSSSSSSRPPTRA 60

Qy 61 RGAPSPGVLPNHAASEPOLAPACTPPAAYVGPGRPPSPQREPORVSHQFRALQLVVD 120

Db 61 RGAPSPGVLPNHAASEPOLAPACTPPAAYVGPGRPPSPQREPORVSHQFRALQLVVD 120

Qy 121 PGDPRSYLDNFIKIGESTGIVCIATVRSSGKLVAVKMDLRKQORRELLFNEVVI RNDY 180

Db 121 PGDPRSYLDNFIKIGESTGIVCIATVRSSGKLVAVKMDLRKQORRELLFNEVVI RNDY 180

Qy 181 QHENVEMVNSYLVGDELWVMEFLBEGALTDIYTHTRMNEBOIAVCLAVLQALSTVLAH 240

Db 181 QHENVEMVNSYLVGDELWVMEFLBEGALTDIYTHTRMNEBOIAVCLAVLQALSTVLAH 240

Qy 241 QGVTHRIKSDSILLTHDGRVKLSDFGCAQVSKVPRRSKLVGTPYMAAPELISRLPYG 300

Db 241 QGVTHRIKSDSILLTHDGRVKLSDFGCAQVSKVPRRSKLVGTPYMAAPELISRLPYG 300

Qy 301 PEVDWISLGIWVEMVDGEPYFNEPPLKAMKMI RDNLPRLKNLHKVSPSLKGF LDRLL 360

Db 301 PEVDWISLGIWVEMVDGEPYFNEPPLKAMKMI RDNLPRLKNLHKVSPSLKGF LDRLL 360

Qy 361 VRDPAQRATAAEILKHPFLAKAGPPASIVPLMRQNRTR 398

Db 361 VRDPAQRATAAEILKHPFLAKAGPPASIVPLMRQNRTR 398

RESULT 3

US-09-082-737-2

Sequence 2, Application US/09082737

Patent No. 6013500

GENERAL INFORMATION:

APPLICANT: Minden, Audrey

TITLE OF INVENTION: PAK4; A No. 6013500e1 Gene Encoding A Serine/

TITLE OF INVENTION: Threonine Kinase

NUMBER OF SEQUENCES: 12

CORRESPONDENCE ADDRESS:

ADDRESSEE: Cooper & Dunham LLP

STREET: 1185 Avenue of the Americas

CITY: New York

STATE: New York

COUNTRY: U.S.A.

ZIP: 11230

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: IBM PC compatible

SOFTWARE: Patentln Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/082,737

FILING DATE:

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: White, John P.

REGISTRATION NUMBER: 28,678

REFERENCE/DOCKET NUMBER: 0575/55311

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 278-0400

TELEFAX: (212) 391-0525

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 591 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-09-082-737-2

Query Match 100.0%; Score 2073; DB 3; Length 591;
Best Local Similarity 100.0%; Pred. No. 3e-155;

Matches 398; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ASGAKLAAGRPNTYPPRADTDHPSRGAQGEPHDVAENGPSAGGLATPQSSSSSSRPPTRA 60

Db 194 ASGAKLAAGRPNTYPPRADTDHPSRGAQGEPHDVAENGPSAGGLATPQSSSSSSRPPTRA 253

Qy 61 RGAPSPGVLPNHAASEPOLAPACTPPAAYVGPGRPPSPQREPORVSHQFRALQLVVD 120

Db 254 RGAPSPGVLPNHAASEPOLAPACTPPAAYVGPGRPPSPQREPORVSHQFRALQLVVD 313

Qy 121 PGDPRSYLDNFIKIGESTGIVCIATVRSSGKLVAVKMDLRKQORRELLFNEVVI RNDY 180

Db 314 PGDPRSYLDNFIKIGESTGIVCIATVRSSGKLVAVKMDLRKQORRELLFNEVVI RNDY 373

Qy 181 QHENVEMVNSYLVGDELWVMEFLBEGALTDIYTHTRMNEBOIAVCLAVLQALSTVLAH 240

Db 374 QHENVEMVNSYLVGDELWVMEFLBEGALTDIYTHTRMNEBOIAVCLAVLQALSTVLAH 433

Qy 241 QGVTHRIKSDSILLTHDGRVKLSDFGCAQVSKVPRRSKLVGTPYMAAPELISRLPYG 300

Db 434 QGVTHRIKSDSILLTHDGRVKLSDFGCAQVSKVPRRSKLVGTPYMAAPELISRLPYG 493

Qy 301 PEVDWISLGIWVEMVDGEPYFNEPPLKAMKMI RDNLPRLKNLHKVSPSLKGF LDRLL 360

Db 494 PEVDWISLGIWVEMVDGEPYFNEPPLKAMKMI RDNLPRLKNLHKVSPSLKGF LDRLL 553

Qy 361 VRDPAQRATAAEILKHPFLAKAGPPASIVPLMRQNRTR 398

Db 554 VRDPAQRATAAEILKHPFLAKAGPPASIVPLMRQNRTR 591

RESULT 4

US-09-688-188B-103

Sequence 103, Application US/09688188B

Patent No. 6656716

GENERAL INFORMATION:

APPLICANT: PLOMMAN, GREGORY

APPLICANT: MARTINEZ, RICARDO

APPLICANT: WHITE, DAVID

TITLE OF INVENTION: STE20-RELATED PROTEIN KINASES

FILE REFERENCE: 038602/0328

CURRENT APPLICATION NUMBER: US/09/688,188B

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 17, 2005, 10:04:33 ; Search time 86.0506 Seconds

(Without alignments)
2873.660 Million cell updates/sec

Title: US-10-725-121A-103

Perfect score: 3090

Sequence: 1 MFGRKKRVISAPNSNEHR.....LAKAGPPASTVPLMKQRNTR 591

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867879 seqs, 418409474 residues

Total number of hits satisfying chosen parameters: 1867879

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
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7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep.*
10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep.*
11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
12: /cgn2_6/ptodata/1/pubpaa/US09C_NEW_PUB.pep.*
13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/1/pubpaa/US10E_PUBCOMB.pep.*
17: /cgn2_6/ptodata/1/pubpaa/US10F_PUBCOMB.pep.*
18: /cgn2_6/ptodata/1/pubpaa/US10G_NEW_PUB.pep.*
19: /cgn2_6/ptodata/1/pubpaa/US11A_PUBCOMB.pep.*
20: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
21: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
22: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|---------------------|
| 1 | 3090 | 100.0 | 591 | 10 | US-09-291-417-103 |
| 2 | 3090 | 100.0 | 591 | 14 | US-10-134-102-4 |
| 3 | 3090 | 100.0 | 591 | 15 | US-10-394-322A-48 |
| 4 | 3090 | 100.0 | 591 | 15 | US-10-693-367-2 |
| 5 | 3090 | 100.0 | 591 | 16 | US-10-725-329-103 |
| 6 | 3090 | 100.0 | 591 | 17 | US-10-893-025-5 |
| 7 | 3090 | 100.0 | 591 | 18 | US-10-725-121-103 |
| 8 | 3090 | 100.0 | 591 | 18 | US-10-509-599-18 |
| 9 | 3090 | 100.0 | 620 | 18 | US-10-450-763-49667 |
| 10 | 3075 | 99.5 | 588 | 14 | US-10-134-102-1 |
| 11 | 2860 | 92.6 | 593 | 16 | US-10-618-941-111 |

| | | | | | | |
|----|--------|------|-----|----|-------------------|--------------------|
| 12 | 2073 | 67.1 | 398 | 10 | US-09-291-417-30 | Sequence 30, App1 |
| 13 | 2073 | 67.1 | 398 | 16 | US-10-725-329-30 | Sequence 30, App1 |
| 14 | 2073 | 67.1 | 398 | 18 | US-10-725-121-30 | Sequence 30, App1 |
| 15 | 1748 | 56.6 | 719 | 14 | US-10-331-095-2 | Sequence 2, App1 |
| 16 | 1731 | 56.0 | 719 | 15 | US-10-331-095-4 | Sequence 4, App1 |
| 17 | 1731 | 56.0 | 719 | 15 | US-10-394-322A-49 | Sequence 49, App1 |
| 18 | 1502 | 48.6 | 292 | 15 | US-10-406-676-5 | Sequence 5, App1 |
| 19 | 1502 | 48.6 | 292 | 15 | US-10-406-676-6 | Sequence 6, App1 |
| 20 | 1502 | 48.6 | 292 | 15 | US-10-406-676-8 | Sequence 8, App1 |
| 21 | 1502 | 48.6 | 292 | 15 | US-10-406-676-9 | Sequence 9, App1 |
| 22 | 1502 | 48.6 | 292 | 15 | US-10-406-676-10 | Sequence 10, App1 |
| 23 | 1502 | 48.6 | 292 | 15 | US-10-406-676-11 | Sequence 11, App1 |
| 24 | 1502 | 48.6 | 293 | 15 | US-10-406-676-4 | Sequence 4, App1 |
| 25 | 1487.5 | 48.5 | 639 | 14 | US-10-134-102-6 | Sequence 6, App1 |
| 26 | 1494.5 | 48.4 | 635 | 14 | US-10-134-102-2 | Sequence 2, App1 |
| 27 | 1481 | 47.9 | 292 | 15 | US-10-406-676-7 | Sequence 7, App1 |
| 28 | 1481 | 47.9 | 292 | 15 | US-10-406-676-12 | Sequence 12, App1 |
| 29 | 1473.5 | 47.7 | 681 | 10 | US-09-291-417-29 | Sequence 29, App1 |
| 30 | 1473.5 | 47.7 | 681 | 16 | US-10-725-329-29 | Sequence 29, App1 |
| 31 | 1473.5 | 47.7 | 681 | 16 | US-10-737-450-108 | Sequence 108, App1 |
| 32 | 1473.5 | 47.7 | 681 | 16 | US-10-885-921-10 | Sequence 10, App1 |
| 33 | 1473.5 | 47.7 | 681 | 18 | US-10-725-121-29 | Sequence 29, App1 |
| 34 | 1470.5 | 47.6 | 681 | 10 | US-09-765-815-2 | Sequence 2, App1 |
| 35 | 1467 | 47.5 | 682 | 18 | US-10-840-512-209 | Sequence 209, App1 |
| 36 | 1421 | 46.0 | 292 | 15 | US-10-406-676-15 | Sequence 15, App1 |
| 37 | 1335.5 | 43.2 | 641 | 15 | US-10-311-034-15 | Sequence 15, App1 |
| 38 | 1303 | 42.2 | 290 | 15 | US-10-406-676-13 | Sequence 13, App1 |
| 39 | 1289 | 41.7 | 290 | 15 | US-10-406-676-14 | Sequence 14, App1 |
| 40 | 1289 | 41.7 | 290 | 15 | US-10-406-676-16 | Sequence 16, App1 |
| 41 | 1289 | 41.7 | 290 | 15 | US-10-406-676-17 | Sequence 17, App1 |
| 42 | 1277 | 41.3 | 250 | 15 | US-10-693-367-3 | Sequence 3, App1 |
| 43 | 1213 | 39.3 | 290 | 15 | US-10-406-676-18 | Sequence 18, App1 |
| 44 | 1209 | 39.1 | 290 | 15 | US-10-406-676-19 | Sequence 19, App1 |
| 45 | 1209 | 39.1 | 290 | 15 | US-10-406-676-20 | Sequence 20, App1 |

ALIGNMENTS

RESULT 1
US-09-291-417-103
Sequence 103, Application US/09291417A
Publication No. US2003050230A1
GENERAL INFORMATION:
APPLICANT: PLOOMMAN, GREGORY
APPLICANT: MARTINEZ, RICARDO
APPLICANT: WHYTE, DAVID
TITLE OR INVENTION: STE20-RELATED PROTEIN KINASES
FILE REFERENCE: 240/300
CURRENT APPLICATION NUMBER: US/09/291,417A
CURRENT FILING DATE: 1999-04-13
EARLIER APPLICATION NUMBER: 60/081,784
EARLIER FILING DATE: 1998-04-14
NUMBER OF SEQ ID NOS: 147
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 103
LENGTH: 591
TYPE: PRT
ORGANISM: Full Length Mammalian (Human) PAKShu
US-09-291-417-103

| | | | | |
|-----------------------|----------------|--|----------|------------|
| Query Match | 100.0% | Score 3090 | DB 10 | Length 591 |
| Best Local Similarity | 100.0% | Pred. No. 7.5e-161 | | |
| Matches 591 | Conservative 0 | Mismatch 0 | Indels 0 | Gaps 0 |
| QY | 1 | MFGRKKRVISAPNSNEHRVHTGPDHOKFTGLPRWOSLIESARRKPLVDPACIT | 60 | |
| DB | 1 | MFGRKKRVISAPNSNEHRVHTGPDHOKFTGLPRWOSLIESARRKPLVDPACIT | 60 | |
| QY | 61 | SIOPGAPKTIIVRSKGAQKQALTLIDFEFNNSVTSNSLRDSDPPPARQENGMPZEE | 120 | |
| DB | 61 | SIOPGAPKTIIVRSKGAQKQALTLIDFEFNNSVTSNSLRDSDPPPARQENGMPZEE | 120 | |

QY 121 PATTARGPAGKAGRGFPAGHSEAGSGGDRRRRAGPEKRPKSSREGSGGPQESSRDKRL 180
DB 121 PATTARGPAGKAGRGFPAGHSEAGSGGDRRRRAGPEKRPKSSREGSGGPQESSRDKRL 180
QY 181 SGPVGTGPPAGLASGAKLAAGRPFNTYPRADTDHPSRGAQGEPHDVA PNGPSAGGLAIP 240
DB 181 SGPVGTGPPAGLASGAKLAAGRPFNTYPRADTDHPSRGAQGEPHDVA PNGPSAGGLAIP 240
QY 241 QSSSSSRPPTRRAGAPSPGVLPAGHSEAGSGGDRRRRAGPEKRPKSSREGSGGPQESSRDKRL 300
DB 241 QSSSSSRPPTRRAGAPSPGVLPAGHSEAGSGGDRRRRAGPEKRPKSSREGSGGPQESSRDKRL 300
QY 301 HEOPRALQVLVDPGDRSYLDNFITKIGESTGIVCIATVRSSGKLVAVKMDLRKQOR 360
DB 301 HEOPRALQVLVDPGDRSYLDNFITKIGESTGIVCIATVRSSGKLVAVKMDLRKQOR 360
QY 361 ELTFNEVIMRDYQHEHNVEMTNSYLVDGLMVMMELEGALTDIYTHTRMNEQJIAAV 420
DB 361 ELTFNEVIMRDYQHEHNVEMTNSYLVDGLMVMMELEGALTDIYTHTRMNEQJIAAV 420
QY 421 CLAVLQALSVLHAQGVTHRDIKSDSILLTHDGRVKLSDFGCAQVSKVPRRSKLVGTPY 480
DB 421 CLAVLQALSVLHAQGVTHRDIKSDSILLTHDGRVKLSDFGCAQVSKVPRRSKLVGTPY 480
QY 481 WMAPELISRLPYGPEVDIWSLGIWVEMVDEPPYFNEPPLKAMKMTLDNLPPRLKXHLK 540
DB 481 WMAPELISRLPYGPEVDIWSLGIWVEMVDEPPYFNEPPLKAMKMTLDNLPPRLKXHLK 540
QY 541 VSPBLKGFLLRLVLRDPAGRATAAELLKHPFLAKAGPAPASIVPLMRQNRTR 591
DB 541 VSPBLKGFLLRLVLRDPAGRATAAELLKHPFLAKAGPAPASIVPLMRQNRTR 591

RESULT 2

US-10-134-102-4
; Sequence 4, Application US/10134102
; Publication No. US20030186254A1
; GENERAL INFORMATION:
; APPLICANT: Melnick, Michael B.
; APPLICANT: Moritz, Albrecht
; APPLICANT: Comb, Michael J.
; TITLE OF INVENTION: Regulation of HIV-Tat and Nef by the Pak4 kinase and its
; FILE REFERENCE: CST-176 CIP
; CURRENT APPLICATION NUMBER: US/10/134,102
; PRIOR FILING DATE: 2002-04-29
; PRIOR APPLICATION NUMBER: 09/750,457
; PRIOR FILING DATE: 2000-12-28
; PRIOR APPLICATION NUMBER: 60/173,939
; PRIOR FILING DATE: 1999-12-30
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 591
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-134-102-4

Query Match 100.0%; Score 3090; DB 14; Length 591;

Best Local Similarity 100.0%; Pred. No. 7.5e-161; Mismatches 0; Indels 0; Gaps 0;

Matches 591; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MFGKRRKRVETSAISNFEHRYHTGPDHQQFTGLPRQMSLIESARRPKPLVDPACT 60
DB 1 MFGKRRKRVETSAISNFEHRYHTGPDHQQFTGLPRQMSLIESARRPKPLVDPACT 60
QY 61 SIQGAPKTIYRSGKAGDGLTLLDDEFENSVYTRNSLRDSDPPPARARQENGMEE 120
DB 61 SIQGAPKTIYRSGKAGDGLTLLDDEFENSVYTRNSLRDSDPPPARARQENGMEE 120
QY 121 PATTARGPAGKAGRGFPAGHSEAGSGGDRRRRAGPEKRPKSSREGSGGPQESSRDKRL 180
DB 121 PATTARGPAGKAGRGFPAGHSEAGSGGDRRRRAGPEKRPKSSREGSGGPQESSRDKRL 180
QY 181 SGPVGTGPPAGLASGAKLAAGRPFNTYPRADTDHPSRGAQGEPHDVA PNGPSAGGLAIP 240
DB 181 SGPVGTGPPAGLASGAKLAAGRPFNTYPRADTDHPSRGAQGEPHDVA PNGPSAGGLAIP 240
QY 241 QSSSSSRPPTRRAGAPSPGVLPAGHSEAGSGGDRRRRAGPEKRPKSSREGSGGPQESSRDKRL 300
DB 241 QSSSSSRPPTRRAGAPSPGVLPAGHSEAGSGGDRRRRAGPEKRPKSSREGSGGPQESSRDKRL 300

QY 181 SGPVGTGPPAGLASGAKLAAGRPFNTYPRADTDHPSRGAQGEPHDVA PNGPSAGGLAIP 240
DB 181 SGPVGTGPPAGLASGAKLAAGRPFNTYPRADTDHPSRGAQGEPHDVA PNGPSAGGLAIP 240
QY 241 QSSSSSRPPTRRAGAPSPGVLPAGHSEAGSGGDRRRRAGPEKRPKSSREGSGGPQESSRDKRL 300
DB 241 QSSSSSRPPTRRAGAPSPGVLPAGHSEAGSGGDRRRRAGPEKRPKSSREGSGGPQESSRDKRL 300
QY 301 HEOPRALQVLVDPGDRSYLDNFITKIGESTGIVCIATVRSSGKLVAVKMDLRKQOR 360
DB 301 HEOPRALQVLVDPGDRSYLDNFITKIGESTGIVCIATVRSSGKLVAVKMDLRKQOR 360
QY 361 ELTFNEVIMRDYQHEHNVEMTNSYLVDGLMVMMELEGALTDIYTHTRMNEQJIAAV 420
DB 361 ELTFNEVIMRDYQHEHNVEMTNSYLVDGLMVMMELEGALTDIYTHTRMNEQJIAAV 420
QY 421 CLAVLQALSVLHAQGVTHRDIKSDSILLTHDGRVKLSDFGCAQVSKVPRRSKLVGTPY 480
DB 421 CLAVLQALSVLHAQGVTHRDIKSDSILLTHDGRVKLSDFGCAQVSKVPRRSKLVGTPY 480
QY 481 WMAPELISRLPYGPEVDIWSLGIWVEMVDEPPYFNEPPLKAMKMTLDNLPPRLKXHLK 540
DB 481 WMAPELISRLPYGPEVDIWSLGIWVEMVDEPPYFNEPPLKAMKMTLDNLPPRLKXHLK 540
QY 541 VSPBLKGFLLRLVLRDPAGRATAAELLKHPFLAKAGPAPASIVPLMRQNRTR 591
DB 541 VSPBLKGFLLRLVLRDPAGRATAAELLKHPFLAKAGPAPASIVPLMRQNRTR 591

RESULT 3

US-10-394-322A-48
; Sequence 48, Application US/10394322A
; Publication No. US20030232391A1
; GENERAL INFORMATION:
; APPLICANT: SUNESIS PHARMACEUTICALS, INC.
; APPLICANT: Prescott, John C.
; TITLE OF INVENTION: IDENTIFICATION OF KINASE INHIBITORS
; FILE REFERENCE: 39750-0006 US
; CURRENT APPLICATION NUMBER: US/10/394,322A
; PRIOR FILING DATE: 2003-03-20
; PRIOR APPLICATION NUMBER: US 60/366,892
; PRIOR FILING DATE: 2002-03-21
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 48
; LENGTH: 591
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-394-322A-48

Query Match 100.0%; Score 3090; DB 15; Length 591;

Best Local Similarity 100.0%; Pred. No. 7.5e-161; Mismatches 0; Indels 0; Gaps 0;

Matches 591; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MFGKRRKRVETSAISNFEHRYHTGPDHQQFTGLPRQMSLIESARRPKPLVDPACT 60
DB 1 MFGKRRKRVETSAISNFEHRYHTGPDHQQFTGLPRQMSLIESARRPKPLVDPACT 60
QY 61 SIQGAPKTIYRSGKAGDGLTLLDDEFENSVYTRNSLRDSDPPPARARQENGMEE 120
DB 61 SIQGAPKTIYRSGKAGDGLTLLDDEFENSVYTRNSLRDSDPPPARARQENGMEE 120
QY 121 PATTARGPAGKAGRGFPAGHSEAGSGGDRRRRAGPEKRPKSSREGSGGPQESSRDKRL 180
DB 121 PATTARGPAGKAGRGFPAGHSEAGSGGDRRRRAGPEKRPKSSREGSGGPQESSRDKRL 180
QY 181 SGPVGTGPPAGLASGAKLAAGRPFNTYPRADTDHPSRGAQGEPHDVA PNGPSAGGLAIP 240
DB 181 SGPVGTGPPAGLASGAKLAAGRPFNTYPRADTDHPSRGAQGEPHDVA PNGPSAGGLAIP 240
QY 241 QSSSSSRPPTRRAGAPSPGVLPAGHSEAGSGGDRRRRAGPEKRPKSSREGSGGPQESSRDKRL 300
DB 241 QSSSSSRPPTRRAGAPSPGVLPAGHSEAGSGGDRRRRAGPEKRPKSSREGSGGPQESSRDKRL 300

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 17, 2005, 10:09:48 ; Search time 136.844 Seconds
(without alignments)
2211.556 Million cell updates/sec

Title: US-10-725-121A-103

Perfect score: 3090

Sequence: 1 MRCRKRKRVRISAPSNFHR.....LAKAGPPASIVPLMRQNRTR 591

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database: UniProt 03:*

1: uniprot_sprot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|--------|-------------|--------|-------|-------------|
| 1 | 3090 | 100.0 | 591 | 1 | PAK4_HUMAN |
| 2 | 2860 | 92.6 | 593 | 1 | PAK4_MOUSE |
| 3 | 2856 | 92.4 | 597 | 2 | Q6ZPX0 |
| 4 | 2853 | 92.3 | 593 | 2 | Q80Z97 |
| 5 | 2558 | 82.8 | 501 | 2 | Q8N4E1 |
| 6 | 2202.5 | 71.3 | 438 | 2 | Q8NDE3 |
| 7 | 2202.5 | 71.3 | 467 | 2 | Q9UIS8 |
| 8 | 2124.5 | 68.8 | 650 | 2 | Q90M62 |
| 9 | 2031 | 65.7 | 663 | 2 | Q6GM11 |
| 10 | 1967 | 63.7 | 407 | 2 | Q8K0U2 |
| 11 | 1748 | 56.6 | 719 | 2 | Q8C0U5 |
| 12 | 1745 | 56.5 | 711 | 2 | Q6NVJ4 |
| 13 | 1740 | 56.3 | 719 | 2 | Q8BVD0 |
| 14 | 1731 | 56.0 | 719 | 1 | PAK7_HUMAN |
| 15 | 1731 | 56.0 | 719 | 2 | Q8TBS9 |
| 16 | 1730 | 56.0 | 719 | 2 | Q6RMS7 |
| 17 | 1501.5 | 48.6 | 639 | 1 | PAKM_DROME |
| 18 | 1473.5 | 47.7 | 681 | 1 | PAK6_HUMAN |
| 19 | 1464.5 | 47.4 | 558 | 2 | Q70G55 |
| 20 | 1241 | 40.2 | 240 | 2 | Q8NC85 |
| 21 | 1160 | 37.5 | 229 | 2 | Q9CS71 |
| 22 | 1096.5 | 35.5 | 540 | 2 | Q9U3M1 |
| 23 | 1090.5 | 35.3 | 542 | 2 | Q18637 |
| 24 | 948.5 | 30.7 | 704 | 2 | Q70D76 |
| 25 | 937.5 | 30.3 | 704 | 2 | Q24190 |
| 26 | 937.5 | 30.3 | 704 | 2 | Q9V113 |
| 27 | 936 | 30.3 | 827 | 2 | Q6IWM3 |
| 28 | 932.5 | 30.2 | 704 | 2 | Q24213 |
| 29 | 924 | 29.9 | 544 | 2 | Q8K1R6 |
| 30 | 917 | 29.7 | 544 | 1 | PAK3_RAT |
| 31 | 907 | 29.4 | 577 | 2 | Q803Z0 |

| | | | | | |
|----|-------|------|-----|---|------------|
| 32 | 906.5 | 29.3 | 559 | 1 | PAK3_MOUSE |
| 33 | 905 | 29.3 | 577 | 2 | Q6P0I7 |
| 34 | 904 | 29.3 | 524 | 1 | PAK2_HUMAN |
| 35 | 903 | 29.2 | 564 | 2 | Q8AXB4 |
| 36 | 900 | 29.1 | 524 | 1 | PAK2_RABIT |
| 37 | 895 | 29.0 | 524 | 1 | PAK2_MOUSE |
| 38 | 895 | 29.0 | 524 | 1 | PAK2_RAT |
| 39 | 894 | 28.9 | 524 | 2 | Q6ISC3 |
| 40 | 894 | 28.9 | 544 | 1 | PAK1_RAT |
| 41 | 892.5 | 28.9 | 545 | 1 | PAK1_HUMAN |
| 42 | 891.5 | 28.9 | 559 | 1 | PAK3_HUMAN |
| 43 | 891.5 | 28.9 | 559 | 1 | PAK3_PONTR |
| 44 | 891.5 | 28.9 | 559 | 1 | PAK3_PONPY |
| 45 | 890 | 28.8 | 517 | 2 | Q8AW67 |

ALIGNMENTS

RESULT 1

| PAK4_HUMAN | STANDARD; | PRT; | 591 AA. |
|------------|--|------|---------|
| AC | Q96013; Q9BUJ3; | | |
| DT | 16-OCT-2001 (Ref. 40, Created) | | |
| DT | 16-OCT-2001 (Ref. 40, Last sequence update) | | |
| DT | 05-JUL-2004 (Ref. 44, Last annotation update) | | |
| DE | Serine/threonine-protein kinase PAK 4 (EC 2.7.1.37) (p21-activated kinase 4) (PAK-4). | | |
| GN | Name=PAK4; | | |
| OS | Homo sapiens (Human). | | |
| OC | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; | | |
| OC | Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo. | | |
| OX | NCBI_TaxID=9606; | | |
| RN | [1] | | |
| RP | SEQUENCE FROM N.A. (ISOFORM 1). | | |
| RX | MDLINB=99043860; PubMed=9825598; DOI=10.1093/emboj/17.22.6527; | | |
| RA | Abo A., Qu J., Cammarano M.S., Dan C., Fritsch A., Baud V., | | |
| RA | Belisle B., Minden A., | | |
| RT | "PAK4, a novel effector for Cdc42Hs, is implicated in the reorganization of the actin cytoskeleton and in the formation of filopodia." | | |
| RT | EMBO J. 17:6527-6540(1998). | | |
| RL | [2] | | |
| RN | SEQUENCE FROM N.A. (ISOFORM 1). | | |
| RP | SEQUENCE FROM N.A. (ISOFORM 1). | | |
| RA | Meinick M.B.; | | |
| RA | Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases. | | |
| RN | [3] | | |
| RP | SEQUENCE FROM N.A. (ISOFORMS 1 AND 2). | | |
| RC | TISSUE=Eye, Pancreas, and Placenta; | | |
| RX | MDLINB=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899; | | |
| RA | Straussberg R.L., Feingold E.A., Grouse L.H., Derge J.G., | | |
| RA | Klausner R.D., Collins F.S., Wagner L., Shenmen R.D., Mullany S.J., | | |
| RA | Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Hsieh F., | | |
| RA | Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., | | |
| RA | Diatchenko L., Marishta K., Farmer A.A., Rubin G.M., Hong L., | | |
| RA | Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., | | |
| RA | Brownstein M., Udell T.B., Tothiyuki S., Carninci P., Prange C., | | |
| RA | Raha S.S., Loguettano N.A., Peters G.J., Abramson R.D., Mullany S.J., | | |
| RA | Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., | | |
| RA | Butterfield Y.S.N., Krzyzanski M.I., Skalska U., Small D.E., | | |
| RA | Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., | | |
| RA | Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A., | | |
| RA | Whiting M., Madan A., Young A.C., Green E.D., Dickson M.C., | | |
| RA | Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C., | | |
| RA | Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., | | |
| RA | Butterfield Y.S.N., Krzyzanski M.I., Skalska U., Small D.E., | | |
| RA | Schneerch A., Schein J.E., Jones S.T.M., Marra M.A., | | |
| RT | "Generation and initial analysis of more than 15,000 full-length human | | |
| RT | and mouse cDNA sequences." | | |
| RL | Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002). | | |
| CC | -1- FUNCTION: Activates the JNK pathway. Implicated in the reorganization of the actin cytoskeleton and in the formation of filopodia. | | |

```

CC -1- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC -1- SUBUNIT: Interacts tightly with GTP-bound but not GPP-bound
CC CDC42/p21 and weakly with RAC1.
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named Isoforms=2;
CC Name=1;
CC IsoId=096013-1; Sequence=Displayed;
CC Name=2;
CC IsoId=096013-2; Sequence=VSP_004892, VSP_004893;
CC Note=Experimental confirmation available;
CC TISSUE SPECIFICITY: Highest expression in prostate, testis and
CC colon.
CC -1- PTM: Autophosphorylated when activated by CDC42/p21.
CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family. STE20
CC subfamily.
CC -1- SIMILARITY: Contains 1 CRIB domain.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (see http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AJ011855; CA09820.1; -
DR EMBL; AF005046; AA001210.1; -
DR EMBL; BC002921; AA002921.1; -
DR EMBL; BC011368; AA011368.1; -
DR EMBL; BC025282; AA025282.1; -
DR NSSP; Q13153; 1F3M.
DR Gene; HGNC:16059; PAK4.
DR H-invDB; HIX0015110; -
DR MIM; 605451; -
DR GO; GO:0005794; C:Golgi apparatus; TAS.
DR GO; GO:0006928; P:cell motility; TAS.
DR GO; GO:0007165; P:signal transduction; TAS.
DR InterPro; IPRO11009; Kinase like.
DR InterPro; IPRO00095; PAKbox/rho-binding.
DR InterPro; IPRO00719; Prot_Kinase.
DR InterPro; IPRO08271; Ser_Thr_Pkin_AS.
DR InterPro; IPRO02290; Ser_Thr_Pkinase.
DR InterPro; IPRO11026; WSP_C.
DR Pfam; PF00786; PBD; 1.
DR Pfam; PF00069; Pkinase; 1.
DR ProDom; PD000001; Prot_Kinase; 1.
DR SMART; SM00285; PBD; 1.
DR SMART; SM00220; S_TKC; 1.
DR PROSITE; PS50108; CRIB; 1.
DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
DR PROSITE; PS50011; PROTEIN KINASE DOM; 1.
DR PROSITE; PS00108; PROTEIN KINASE_ST; FALSE_NEG.
KW Alternative splicing; ATP-binding; Phosphorylation;
KW Serine/threonine-protein kinase; Transferase.
FT DOMAIN 11 24 CRIB.
FT DOMAIN 25 320 linker.
FT DOMAIN 321 572 Protein kinase.
FT NP_BIND 327 335 ATP (By similarity).
FT BINDING 350 350 ATP (By similarity).
FT ACT_SITE 440 440 Proton acceptor (By similarity).
FT VARSPIC 120 120 E -> K (in isoform 2).
FT VARSPIC 121 285 /Frtid=VSP_004892.
FT VARSPIC 121 285 /Frtid=VSP_004893.
FT VARSPIC 121 285 /Frtid=VSP_004893.
SQ SEQUENCE 591 AA; 64071 MW; 04C2A5C0B06427D5 CRC64;
Query Match 100.0%; Score 3090; DB 1; Length 591;
Best Local Similarity 100.0%; Pred. No. 3,7e-106;
Matches 591; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
1 MFGRKRRVEISAPSEFHRVHTGPDQKQFTGLPRQWGLIESSARRPKPLVDPACT 60
1 MFGKRRKRVETISAPSEFHRVHTGPDQKQFTGLPRQWGLIESSARRPKPLVDPACT 60

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QY 61 SIQGAPEKTVRGSKGAKGALTLTLDPEFNMSTVTRNSLSLRDPPPPARAOENGMBE 120
DB 61 SIQGAPEKTVRGSKGAKGALTLTLDPEFNMSTVTRNSLSLRDPPPPARAOENGMBE 120
QY 121 PATTARPGPKAGSRGRFAGHSEAGGSGGRRRAGPEKRPKSRREGSGPQESRDRL 180
DB 121 PATTARPGPKAGSRGRFAGHSEAGGSGGRRRAGPEKRPKSRREGSGPQESRDRL 180
QY 181 SGPDVGTTPQAGLASGKLAAGRPFTYPRADTDHPSRGAQGEHVDVAPGPSAGLAIP 240
DB 181 SGPDVGTTPQAGLASGKLAAGRPFTYPRADTDHPSRGAQGEHVDVAPGPSAGLAIP 240
QY 241 QSSSSSRPPTRRAGAPSPVLPGRPHASEPOLAPACTPAAPAVPGPPSPQEPORVS 300
DB 241 QSSSSSRPPTRRAGAPSPVLPGRPHASEPOLAPACTPAAPAVPGPPSPQEPORVS 300
QY 301 HEQFRALQVDPGDRSYLDNFIKIGSGSTGICVATYRSSGKLVAVKMDLRKQQR 360
DB 301 HEQFRALQVDPGDRSYLDNFIKIGSGSTGICVATYRSSGKLVAVKMDLRKQQR 360
QY 361 ELIPNEVIRKDYQHEVNVEMNNSYLVGDELWVMEELREGALTDVYTHRMNEEQIAV 420
DB 361 ELIPNEVIRKDYQHEVNVEMNNSYLVGDELWVMEELREGALTDVYTHRMNEEQIAV 420
QY 421 CLAVLQALSVLHAQGVTHRDIKSDSLTTHDGRVYKSDPFCQAVSKVPRKSLVGTPT 480
DB 421 CLAVLQALSVLHAQGVTHRDIKSDSLTTHDGRVYKSDPFCQAVSKVPRKSLVGTPT 480
QY 481 WMAPELISRLPYGEVDIWSLGIWVIMVDGEPPEYFNEPPLKMKIMRDLNPLRLKYLHK 540
DB 481 WMAPELISRLPYGEVDIWSLGIWVIMVDGEPPEYFNEPPLKMKIMRDLNPLRLKYLHK 540
QY 541 VSPBLKGFRLRLVDRDPAQRATAELKHPFLAKAGPPASIVPLMRNRR 591
DB 541 VSPBLKGFRLRLVDRDPAQRATAELKHPFLAKAGPPASIVPLMRNRR 591

RESULT 2
PAK4_MOUSE STANDARD; PRT; 593 AA.
ID PAK4_MOUSE
AC O8BTW9;
DT 05-JUL-2004 (Ref. 44, Created)
DT 05-JUL-2004 (Ref. 44, Last sequence update)
DT 05-JUL-2004 (Ref. 44, Last annotation update)
DE Serine/threonine-protein kinase PAK 4 (EC 2.7.1.37) (p21-activated
DE kinase 4) (PAK-4).
GN Name=PAK4;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NOD; TISSUE=Thymus;
RX MEDLINE=22354683; Pubmed=12466851; DOI=10.1038/nature01266;
RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA Nikaido I., Osato N., Satoh R., Suzuki H., Yamanka I., Kiyosawa H.,
RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojouri T.,
RA Baldarelli R., Hill D.P., Butt C., Hume D.A., Quackenhut J.,
RA Schirml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
RA Blake J.A., Bradt D., Brusic V., Choehia C., Corbani L.E., Cousins S.,
RA Dalla B., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
RA Gaasterland T., Gariboldi M., Glasl C., Godzik A., Gough J.,
RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.U., Jarvis E.D.,
RA Kanai A., Kawai H., Kawasawa Y., Kedzierski R.M., King B.L.,
RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA MacIock D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
RA Nagaishima T., Numata K., Okido T., Pavan W.J., Petras G., Pesole G.,
RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramchandran S.,
RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,
RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,

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OM protein - protein search, using sw model

Run on: November 17, 2005, 10:00:02 ; Search time 31.6714 Seconds

(Without alignments)
1795.441 Million cell updates/sec

Title: US-10-725-121A-103

Perfect score: 3090

Sequence: 1 MFGRKKRKRIVISAPSNFHR.....LAKAGPPASIVPLMRQNR 591

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 79: *
1: PIR1: *
2: PIR2: *
3: PIR3: *
4: PIR4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|--------|-------------|--------|--------|---------------------|
| 1 | 1096.5 | 35.5 | 540 | T19956 | hypothetical prote |
| 2 | 1090.5 | 35.3 | 542 | T19952 | hypothetical prote |
| 3 | 917 | 29.7 | 544 | A57597 | beta-p21-activated |
| 4 | 907 | 29.4 | 544 | I49376 | p21 activated kina |
| 5 | 895.5 | 29.0 | 525 | S58682 | protein kinase, p2 |
| 6 | 892.5 | 28.9 | 545 | G01773 | p21-activated prot |
| 7 | 892 | 28.9 | 544 | S40482 | serine/threonine-s |
| 8 | 846.5 | 27.4 | 1230 | T18259 | probable serine/th |
| 9 | 846.5 | 27.4 | 1230 | T18259 | serine/threonine p |
| 10 | 837 | 27.1 | 939 | S28394 | probable serine/th |
| 11 | 823.5 | 26.7 | 658 | T39500 | serine/threonine-s |
| 12 | 814.5 | 26.4 | 658 | S60170 | protein kinase Pak |
| 13 | 811.5 | 26.3 | 622 | T15467 | hypothetical prote |
| 14 | 760 | 24.6 | 842 | S60402 | protein kinase CLA |
| 15 | 722 | 23.4 | 378 | T26684 | hypothetical prote |
| 16 | 697 | 22.6 | 589 | T38086 | serine/threonine-p |
| 17 | 651.5 | 21.1 | 555 | S51884 | probable protein k |
| 18 | 505 | 16.3 | 836 | B96716 | probable serine/th |
| 19 | 498 | 16.1 | 471 | T39232 | probable serine th |
| 20 | 478 | 15.5 | 1102 | JC6316 | probable protein k |
| 21 | 476 | 15.4 | 819 | T34356 | hypothetical prote |
| 22 | 476 | 15.4 | 819 | A53714 | protein kinase (EC |
| 23 | 470.5 | 15.2 | 829 | T29372 | hypothetical prote |
| 24 | 464 | 15.0 | 436 | S71886 | Ste20-like protein |
| 25 | 463 | 15.0 | 1231 | T18532 | serine/threonine pr |
| 26 | 462 | 15.0 | 1233 | T14157 | serine/threonine p |
| 27 | 460 | 14.9 | 1206 | T34021 | protein kinase SK2 |
| 28 | 458.5 | 14.8 | 690 | C96572 | protein p12M16.4 |
| 29 | 455.5 | 14.7 | 1080 | S48944 | hypothetical prote |

| | | | | | | |
|----|-------|------|------|---|--------|--------------------|
| 30 | 455 | 14.7 | 1233 | 2 | T30989 | serine/threonine p |
| 31 | 450.5 | 14.6 | 312 | 2 | T38525 | serine/threonine p |
| 32 | 445 | 14.4 | 1001 | 2 | T17365 | serine/threonine p |
| 33 | 440.5 | 14.3 | 1075 | 2 | T27623 | hypothetical prote |
| 34 | 440.5 | 14.3 | 1080 | 2 | T27622 | hypothetical prote |
| 35 | 437.5 | 14.2 | 1062 | 2 | S46367 | protein kinase CDC |
| 36 | 428 | 13.9 | 1228 | 2 | T18897 | hypothetical prote |
| 37 | 424.5 | 13.7 | 659 | 1 | A39723 | protein kinase byr |
| 38 | 421 | 13.6 | 553 | 2 | T01479 | hypothetical prote |
| 39 | 419 | 13.6 | 883 | 2 | A96652 | hypothetical prote |
| 40 | 417.5 | 13.5 | 1174 | 2 | T43051 | protein kinase C (|
| 41 | 413 | 13.4 | 561 | 2 | T51417 | protein kinase-lik |
| 42 | 409.5 | 13.3 | 652 | 2 | T39722 | serine/threonine p |
| 43 | 409 | 13.2 | 891 | 2 | T40503 | protein kinase p |
| 44 | 405.5 | 13.1 | 1139 | 1 | S61918 | protein kinase C (|
| 45 | 404.5 | 13.1 | 1135 | 1 | A29813 | 132k ninaC protein |

ALIGNMENTS

| | | | | | | | | | |
|---|-----|---|-----|--|--|--|--|--|--|
| RESULT 1 | | | | | | | | | |
| T19956 | | | | | | | | | |
| hypothetical protein C45B11.1b - Caenorhabditis elegans | | | | | | | | | |
| C/Species: Caenorhabditis elegans | | | | | | | | | |
| C/Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 16-Aug-2004 | | | | | | | | | |
| C/Accession: T19956 | | | | | | | | | |
| R/McMurray, A. | | | | | | | | | |
| submitted to the EMBL Data Library, June 1996 | | | | | | | | | |
| A/Reference number: Z19202 | | | | | | | | | |
| A/Accession: T19956 | | | | | | | | | |
| A/Status: preliminary; translated from GB/EMBL/DBJ | | | | | | | | | |
| A/Molecule type: DNA | | | | | | | | | |
| A/Residues: 1-540 <MTL> | | | | | | | | | |
| A/Cross-references: UNIPROT:O9U3M1; EMBL:Z74029; P1DN:CAA98433.1; GSPDB:GN00023; CESP:CA4 | | | | | | | | | |
| A/Experimental source: clone C45B11 | | | | | | | | | |
| C/Genetic: | | | | | | | | | |
| A/Gene: CESP:C45B11.1b | | | | | | | | | |
| A/Map position: 5 | | | | | | | | | |
| A/Intons: 13/2; 62/3; 104/2; 231/3; 367/2; 468/3 | | | | | | | | | |
| C/Superfamily: protein kinase homology | | | | | | | | | |
| Query Match | | | | | | | | | |
| Best Local Similarity 35.5%; Score 1096.5; DB 2; Length 540; | | | | | | | | | |
| Matches 251; Conservative 67; Mismatches 151; Indels 133; Gaps 9; | | | | | | | | | |
| Qy | 4 | KRKKRVEISAPSNFHRVHTGPDHOKFTGLPRQMSLT--ESARRPPLVDPACTIS | 61 | | | | | | |
| Db | 29 | RKYKSRISITPSNFERIRHAGFDARSGTYTGLPKQNALGPPRSISRPMVDPSCTTP | 88 | | | | | | |
| Qy | 62 | IOPGAPFTIVSGSKAKDGLTLLDFENMSVTRNSLRLRDSPPPARARQRMDEEP | 121 | | | | | | |
| Db | 89 | VDVAELKTVIRGSSRYNSPLPGFMNNSPMPVSARSNSLRISATVSP----- | 135 | | | | | | |
| Qy | 122 | ATTARAGPGKAGSRGPRAGHSEAGSGGDRRRAGPEKRPSSSEGGGPGQESSRDKRPLS | 181 | | | | | | |
| Db | 136 | -----VVNVSASHSFRPLTPVSGR----- | 156 | | | | | | |
| Qy | 182 | GPDVGTTPQAGLASGAKLAAGRPFTYPPRADTDHPSRGAQGEPHDVAHPNGSAGLAIPO | 241 | | | | | | |
| Db | 157 | -----GTFP----- | 170 | | | | | | |
| Qy | 242 | SSSSSRPPTFRAGAPSPGVLGH-----ASBPQLAPPACTPAADAVPQPG | 288 | | | | | | |
| Db | 171 | ---RNQKPPW---STTFGVEKPHQYQOITIVAPSRTPPLQOPKS-----PST | 213 | | | | | | |
| Qy | 289 | PRPQREP---QVSHQEPAAALQVVDGDDPSYDNRFKIGEGSGTGVCIATVNSSSK | 345 | | | | | | |
| Db | 214 | PQMRQPPKTEVSDBEFNNALKFVVDGTPRSDLTLDYKQIGEGSGVVEAAYKISTQ | 273 | | | | | | |
| Qy | 346 | LVAIVKQDRLKQQRRLTFNENVVIMRDYOHENNVEMTNSYLVGDELMVMEFLEGALTD | 405 | | | | | | |
| Db | 274 | IYAVKRMNLKQQRRLTFNENVVIMRDYOHENNVEMTNSYLVGDELMVMEFLEGALTD | 333 | | | | | | |

QY 406 IYHTTRNEBOIAVCLAVLQALSVLHAQGYIHRDIKSDSILLTHDGRVYKLSDEGFCQAV 465
DB 334 IYATRTKTEPQIATISRQVGLALDFLHARKVYIHRDIKSDSILLKRDGTVKLTDGFCGQL 393
QY 466 SKEVPRKSLVGPYPMAPBELISRLPYGPEVDIWSLGIWYIEMVDGEPYFNEBPPLKAMK 525
DB 394 SEEVPRRSLVGPYPMAPBELISRLPYGPEVDIWSLGIWYIEMVDGEPYFNEBPPLKAMK 453
QY 526 MIRDNLPRRLKLNHKVSPSLKGFIDRLVDRDPQARATAAELIKHPLAKAGPPASIVPLM 585
DB 454 RIRDEHARFSRRAKVSVELSELISHCIYKDVNKRMPAKDLRHPFPAKQSHSSIAPL 513
QY 586 RQ 587
DB 514 LQ 515

RESULT 2

T19952
hypothetical protein C45B11.1a - Caenorhabditis elegans
C/Species: Caenorhabditis elegans
C/Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 16-Aug-2004
C/Accession: T19952
R/McMurray, A.
submitted to the EMBL Data Library, June 1996
A/Reference number: Z19202
A/Accession: T19952
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-542 <M1>
A/Cross-references: UNIPROT:Q16637, EMBL:Z74029, PIDN:CA098429.1, GSPDB:GN00023, CBSP:C4
C/Experimental source: clone C45B11
A/Genetic8:
A/Map position: 5
A/Intons: 13/2; 104/2; 233/3; 369/2; 470/3
C/Superfamily: protein kinase homology

Query Match 35.3%; Score 1090.5; DB 2; Length 542;
Best Local Similarity 42.0%; Pred. No. 6.6e-31;
Matches 253; Conservative 69; Mismatches 149; Indels 131; Gaps 11;
QY 4 KRKKRVISAPSPNEHVRHTGPDQHEOKFTGLPRQMSLI--ESARRPKPLVDPACTIS 61
DB 29 RKVKKSISTPSNEHVIHAGFDARSGTYTGLPKQMLDPPRSISRPRKMDVPSCTTP 88
QY 62 IQPGAPRTIVGSKAGKDGALTLLDDEFENMSVTRNSLRDSDPPPARAQAENGMPBEP 121
DB 89 VDVAEKTVIRGP-----SSFRYNSPLP-----FGMTNSP 119
QY 122 ATTARGPGRKAGSGRPAHSEAGSGDRRRAPEKRPKSSREGSGGPOESSNDKPLS 181
DB 120 MPSTV---ASNSLRISATSPVNVSSARHSFRPTLPVPSQR----- 158
QY 182 GPDVGTQPPAGLAAAGRPENTYPRADTDHPSRGAQGEPRHDAVNPGSAGALAPQ 241
DB 159 -----GYFP-----NDSTYAPLPF-- 172
QY 242 SSSSSSPPTRRAGAPPGVLPPI-----ASEPQLAPPACTPAAPVPPGPG 288
DB 173 ---RNGRPPM---STTFGEVKEPHQYQOITIVAPSRITTPQLQPKS-----PST 215
QY 289 PRSPQRDE--QRVSHQGFRAALQVVDGPPRSYLDNFIKIGSGSTGIVCIATVRSAGK 345
DB 216 PQARQOPKCTEGVSDEFNALKFVVDGTPRSDDLTDYKQIGSGSTGVVAAYKISTKQ 275
QY 346 IYAVKCKMDLRKQGRRELFENVIMRDYQHENVEMVNSYLVGDELVMVEFLREGALTD 405
DB 276 IYAVKRNKLRKQGRRELFENVIMRDYQHENVEMVNSYLVGDELVMVEFLREGALTD 335
QY 406 IYHTTRNEBOIAVCLAVLQALSVLHAQGYIHRDIKSDSILLTHDGRVYKLSDEGFCQAV 465

DB 336 IYATRTKTEPQIATISRQVGLALDFLHARKVYIHRDIKSDSILLKRDGTVKLTDGFCGQL 393
QY 466 SKEVPRKSLVGPYPMAPBELISRLPYGPEVDIWSLGIWYIEMVDGEPYFNEBPPLKAMK 525
DB 396 SEEVPRRSLVGPYPMAPBELISRLPYGPEVDIWSLGIWYIEMVDGEPYFNEBPPLKAMK 453
QY 526 MIRDNLPRRLKLNHKVSPSLKGFIDRLVDRDPQARATAAELIKHPLAKAGPPASIVPLM 585
DB 456 RIRDEHARFSRRAKVSVELSELISHCIYKDVNKRMPAKDLRHPFPAKQSHSSIAPL 513
QY 586 RQ 587
DB 516 LQ 517

RESULT 3

A57597
beta-p21-activated protein kinase - rat
N/Alternate names: beta-PAK
C/Species: Rattus norvegicus (Norway rat)
C/Date: 08-Feb-1996 #sequence_revision 08-Feb-1996 #text_change 09-Jul-2004
C/Accession: A57597
R/Manser, B./Chong, C.; Zhao, Z.S.; Leung, T.; Michael, G.; Hall, C.; Lim, L.
J. Biol. Chem. 270, 25070-25078, 1995
A/Title: Molecular cloning of a new member of the p21-Cdc42/Rac-activated kinase (PAK) f
A/Reference number: A57597; MUID:96027610; PMID:7559638
A/Accession: A57597
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-544 <MAN>
A/Cross-references: UNIPROT:Q62829; GB:U33314; NID:G1039424; PIDN:AAC52268.1; PID:G103942
C/Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homolo
C/Keywords: ATP
F/266-519/Domain: protein kinase homology <KIN>
F/274-282/Region: protein kinase ATP-binding motif

Query Match 29.7%; Score 917; DB 2; Length 544;
Best Local Similarity 35.8%; Pred. No. 5.2e-25;
Matches 211; Conservative 87; Mismatches 165; Indels 126; Gaps 8;
QY 4 KRKKRVISAPSPNEHVRHTGPDQHEOKFTGLPRQMSLI--ESARRPKPLVDP 56
DB 63 KEKRPKISLPSPNEHVIHAGFDVAVGSEFTGIDQWARRLQTSNITGLKQKNPOAVLD- 121
QY 57 ACTISIQPGAPRTIVGSKAGKDGALTLLDDEFENMSVTRNSLRDSDPPPARAQAENG 116
DB 122 -----VKEYDSKRYNNQKTMSTP----- 141
QY 117 MPREPATTARAGPKAGSRGRPAHSEAGSGDRRRAPEKRPKSSREGSGGPOESSRD 176
DB 142 -----SGDSSAHGYIAAHQ-----SNTKTASEPPLAPPVSEEDDEBEDEED 184
QY 177 KRPLSGPDVGTQPPAGLAAAGRPENTYPRADTDHPSRGAQGEPRHDAVNPGSAGC 226
DB 185 NEP---PPVLAPEPHEKTS-----IYRSVSESIASPA-----APVKEATPP 223
QY 237 LAIPQSSSSSPPTRRAGAPSPGVLGPHASEPQLAPPACTPAAPVPPGPGPRSPPREP 296
DB 224 SAENANSTLYKRTDR-----ORKK 243
QY 297 QRVSHQGFRAALQVVDGPPRSYLDNFIKIGSGSTGIVCIATVRSAGKLVAVKCKMDLRK 356
DB 244 SKMTDEILKLSIVSGVPKPKYRFEKIGGASGTYTALDIAGQVAILKQMLQ 303
QY 357 QORRELFENVIMRDYQHENVEMVNSYLVGDELVMVEFLREGALTDIVHTTRNEEQ 416
DB 304 QPKKELIINEILVWRBKNENIIVYLDSTYLVGDELVMVEFLREGALTDIVTETCMEGQ 363
QY 417 IYAVCLAVLQALSVLHAQGYIHRDIKSDSILLTHDGRVYKLSDEGFCQAVKEVPRRSSTV 476
DB 364 IYAVCRECLQALPFLSHNOVYIHRDIKSDNILLKDGDSVVKLTDGFCQITPEQSKRTMV 423
QY 477 GTPYPMAPBELISRLPYGPEVDIWSLGIWYIEMVDGEPYFNEBPPLKAMKIRDNLPRLK 536

invention relates to nucleic acid molecule encoding a kinase polypeptide selected from STK2, STK3, STK4, STK5, STK6, STK7, ZC1, ZC2, ZC3, ZC4, KHS2, SUVU1, SUVU3, GSK2, PAK4 and PAK5. The proteins are used to identify agonists and antagonists, and to raise antibodies. The polynucleotides are useful in gene therapy protocols. The polynucleotides, antibodies, antagonists and agonists may be used to treat diseases such as immune-related disorders and diseases (e.g. rheumatoid arthritis, atherosclerosis, chronic inflammatory bowel disease (e.g. Crohn's disease), asthma, osteoarthritis, psoriasis, atherosclerosis, rhinitis, autoimmunity, and organ transplantation, chronic inflammatory disease, multiple sclerosis, organ transplantation, myocardial infarction, cardiovascular disease, stroke, renal failure, oxidative stress-related neurodegenerative disorders (e.g. amyotrophic lateral sclerosis, Parkinson's disease and Leigh syndrome), cancer, cardiomyopathies, ischemic disorders, inflammatory disorders, diabetes mellitus, fibrotic and meangial disorders. The proteins may also be useful for cell growth regulation (e.g. in wound healing), T cell activation, mitosis control, and as immunosuppressants

Sequence 591 AA:

Query Match 100.0%; Score 3090; DB 2; Length 591;
Best Local Similarity 100.0%; Pred. No. 2.8e-216;
Matches 591; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 MFGRRKKRVEISAPSNFEHVRHTGFDQHEQKFTGLPRQWOSLIRESARRPKPLVDPACIT 60
1 MFGRRKKRVEISAPSNFEHVRHTGFDQHEQKFTGLPRQWOSLIRESARRPKPLVDPACIT 60
61 SIQGAPKTIIVRGSKGAKDGLTLTLLDEFENMSYTRNSLRSDPPPPARARQNGMPEE 120
61 SIQGAPKTIIVRGSKGAKDGLTLTLLDEFENMSYTRNSLRSDPPPPARARQNGMPEE 120
121 PATTARAGPGKAGRGKGFAGHSEAGSGSGDRRAKPEKRPSSRESGGPGESSRDKRPL 180
121 PATTARAGPGKAGRGKGFAGHSEAGSGSGDRRAKPEKRPSSRESGGPGESSRDKRPL 180
121 PATTARAGPGKAGRGKGFAGHSEAGSGSGDRRAKPEKRPSSRESGGPGESSRDKRPL 180
121 PATTARAGPGKAGRGKGFAGHSEAGSGSGDRRAKPEKRPSSRESGGPGESSRDKRPL 180
181 SGPVGTGPPAGLASGAKLAAGRPNTYPRADTHPSRGAQGEHVDVAPNGPSAGLAIP 240
181 SGPVGTGPPAGLASGAKLAAGRPNTYPRADTHPSRGAQGEHVDVAPNGPSAGLAIP 240
181 SGPVGTGPPAGLASGAKLAAGRPNTYPRADTHPSRGAQGEHVDVAPNGPSAGLAIP 240
241 QSSSSSRPPTARAGAPSPVLAGPHASEPQLAPACTPPADAVGPPGPPSPQREPORVS 300
241 QSSSSSRPPTARAGAPSPVLAGPHASEPQLAPACTPPADAVGPPGPPSPQREPORVS 300
241 QSSSSSRPPTARAGAPSPVLAGPHASEPQLAPACTPPADAVGPPGPPSPQREPORVS 300
301 HEQFRALQLVVDGDRSYLDNFIKIGSGTGIVCIATYRSSGKLVAVKXMDLRKQORR 360
301 HEQFRALQLVVDGDRSYLDNFIKIGSGTGIVCIATYRSSGKLVAVKXMDLRKQORR 360
301 HEQFRALQLVVDGDRSYLDNFIKIGSGTGIVCIATYRSSGKLVAVKXMDLRKQORR 360
361 ELLENVAVIMRDYGHENVMYNSYLVDGLAVMVEFLGEGALTDIYTHMNEEQIAAV 420
361 ELLENVAVIMRDYGHENVMYNSYLVDGLAVMVEFLGEGALTDIYTHMNEEQIAAV 420
361 ELLENVAVIMRDYGHENVMYNSYLVDGLAVMVEFLGEGALTDIYTHMNEEQIAAV 420
421 CLAVIALSVLAAGVTHRDIKSDSILLTHDGRVGLSDGFCAYSKVPPRKSILVGPY 480
421 CLAVIALSVLAAGVTHRDIKSDSILLTHDGRVGLSDGFCAYSKVPPRKSILVGPY 480
421 CLAVIALSVLAAGVTHRDIKSDSILLTHDGRVGLSDGFCAYSKVPPRKSILVGPY 480
481 WMAEELISRLPYGEBVDIWSIGIWIEMVDEPPFPNPKAMKMRDNI.PPRIKOLHK 540
481 WMAEELISRLPYGEBVDIWSIGIWIEMVDEPPFPNPKAMKMRDNI.PPRIKOLHK 540
541 VSPSLKGFIDRLVLRDPAQRATAAEELKHPLAKAGPASTIVPLMKQRTR 591
541 VSPSLKGFIDRLVLRDPAQRATAAEELKHPLAKAGPASTIVPLMKQRTR 591

RESULT 2
AAV59128
ID AAV59128 standard; protein; 591 AA.

AAV59128,
AC
XX
DT 08-MAR-2000 (first entry)

Human serine/threonine kinase, PAK4.
PAK4, serine/threonine kinase; GTPase; intracellular signal cascade; Rac; Cdc42h; morphogenesis; mitogenesis; JNK; p38 MAP kinase; human; actin polymerization; filopodia; cancer; arthritis.
Homo sapiens.
W09963073-A1.
09-DEC-1999.
21-MAY-1999; 99MO-US011341.
21-MAY-1998; 98US-00082737.
(UYCO) UNIV COLUMBIA NEW YORK.
Minden A;
WPI; 2000-072881/06.
N-PSDB; AAZ40657.
Novel mammalian nucleic acid useful for treating cancer and arthritis.
Claim 8; Fig 1A-B; 95pp; English.

The invention relates to an isolated mammalian nucleic acid that encodes PAK4, a novel serine/threonine kinase or its mutant homolog. PAK4 is an effector for the GTPases Rac and Cdc42h which are involved in intracellular signal cascades, morphogenesis and mitogenesis, and activate the JNK and p38 MAP kinase pathways. Inhibiting interaction of PAK4 with these enzymes will thus result in inhibition of actin polymerization and formation of filopodia. The PAK4 nucleic acid used for recombinant production of the protein, and as a source of probes for identifying homologous sequences and of (anti)sense oligonucleotides for inhibiting PAK4 expression. The protein, or its fragments, are used to raise specific antibodies and these are useful as ligands for therapeutic inhibition of interaction between PAK4 and its native binding partners. Inhibition of PAK4 activity or expression is used for treatment of cancer and arthritis. The present sequence represents the human serine/threonine kinase, PAK4

Sequence 591 AA:

Query Match 100.0%; Score 3090; DB 3; Length 591;
Best Local Similarity 100.0%; Pred. No. 2.8e-216;
Matches 591; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 MFGRRKKRVEISAPSNFEHVRHTGFDQHEQKFTGLPRQWOSLIRESARRPKPLVDPACIT 60
1 MFGRRKKRVEISAPSNFEHVRHTGFDQHEQKFTGLPRQWOSLIRESARRPKPLVDPACIT 60
61 SIQGAPKTIIVRGSKGAKDGLTLTLLDEFENMSYTRNSLRSDPPPPARARQNGMPEE 120
61 SIQGAPKTIIVRGSKGAKDGLTLTLLDEFENMSYTRNSLRSDPPPPARARQNGMPEE 120
121 PATTARAGPGKAGRGKGFAGHSEAGSGSGDRRAKPEKRPSSRESGGPGESSRDKRPL 180
121 PATTARAGPGKAGRGKGFAGHSEAGSGSGDRRAKPEKRPSSRESGGPGESSRDKRPL 180
121 PATTARAGPGKAGRGKGFAGHSEAGSGSGDRRAKPEKRPSSRESGGPGESSRDKRPL 180
121 PATTARAGPGKAGRGKGFAGHSEAGSGSGDRRAKPEKRPSSRESGGPGESSRDKRPL 180
181 SGPVGTGPPAGLASGAKLAAGRPNTYPRADTHPSRGAQGEHVDVAPNGPSAGLAIP 240
181 SGPVGTGPPAGLASGAKLAAGRPNTYPRADTHPSRGAQGEHVDVAPNGPSAGLAIP 240
181 SGPVGTGPPAGLASGAKLAAGRPNTYPRADTHPSRGAQGEHVDVAPNGPSAGLAIP 240
241 QSSSSSRPPTARAGAPSPVLAGPHASEPQLAPACTPPADAVGPPGPPSPQREPORVS 300
241 QSSSSSRPPTARAGAPSPVLAGPHASEPQLAPACTPPADAVGPPGPPSPQREPORVS 300
241 QSSSSSRPPTARAGAPSPVLAGPHASEPQLAPACTPPADAVGPPGPPSPQREPORVS 300
301 HEQFRALQLVVDGDRSYLDNFIKIGSGTGIVCIATYRSSGKLVAVKXMDLRKQORR 360
301 HEQFRALQLVVDGDRSYLDNFIKIGSGTGIVCIATYRSSGKLVAVKXMDLRKQORR 360

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 17, 2005, 09:51:36 / Search time 39.4398 Seconds
(without alignments)
1118.605 Million cell updates/sec

Title: US-10-725-121A-103

Perfect score: 3090
Sequence: 1 MFGRKKRVRISAPSNPEHR.....LAKAGPPASTVPLMRQNRTR 591

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents AA:*
1: /cgn2_6/ptodata/1/1aa/5A COMB .pep:*
2: /cgn2_6/ptodata/1/1aa/5B COMB .pep:*
3: /cgn2_6/ptodata/1/1aa/6A COMB .pep:*
4: /cgn2_6/ptodata/1/1aa/6B COMB .pep:*
5: /cgn2_6/ptodata/1/1aa/PTCUS COMB .pep:*
6: /cgn2_6/ptodata/1/1aa/backfile1.pcp:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|--------|-------------|--------|-----------------------|-------------------|
| 1 | 3090 | 100.0 | 591 | 3 US-09-082-737-2 | Sequence 2, Appl1 |
| 2 | 3090 | 100.0 | 591 | 4 US-09-688-188B-103 | Sequence 103, App |
| 3 | 3090 | 100.0 | 591 | 4 US-09-718-032-2 | Sequence 2, Appl1 |
| 4 | 3090 | 100.0 | 591 | 4 US-09-291-417D-103 | Sequence 103, App |
| 5 | 3090 | 100.0 | 591 | 4 US-09-949-016-6665 | Sequence 6665, Ap |
| 6 | 3090 | 100.0 | 620 | 4 US-09-949-016-7206 | Sequence 7206, Ap |
| 7 | 2073 | 67.1 | 398 | 4 US-09-688-188B-30 | Sequence 30, Appl |
| 8 | 2073 | 67.1 | 398 | 4 US-09-291-417D-30 | Sequence 30, Appl |
| 9 | 1473.5 | 47.7 | 681 | 4 US-09-688-188B-29 | Sequence 29, Appl |
| 10 | 1473.5 | 47.7 | 681 | 4 US-09-291-417D-29 | Sequence 29, Appl |
| 11 | 1473.5 | 47.7 | 684 | 4 US-09-949-016-10445 | Sequence 10445, A |
| 12 | 1470.5 | 47.6 | 681 | 4 US-09-765-815-2 | Sequence 2, Appl1 |
| 13 | 1277 | 41.3 | 250 | 3 US-09-082-737-3 | Sequence 3, Appl1 |
| 14 | 1277 | 41.3 | 250 | 4 US-09-718-032-3 | Sequence 2, Appl1 |
| 15 | 912 | 29.5 | 544 | 2 US-08-935-760-2 | Sequence 11562, A |
| 16 | 909 | 29.4 | 544 | 4 US-09-949-016-11562 | Sequence 95, Appl |
| 17 | 907 | 29.4 | 544 | 4 US-09-688-188B-95 | Sequence 95, Appl |
| 18 | 907 | 29.4 | 544 | 4 US-09-291-417D-95 | Sequence 95, Appl |
| 19 | 904 | 29.3 | 544 | 4 US-09-538-092-1301 | Sequence 1301, Ap |
| 20 | 900 | 29.1 | 524 | 2 US-08-615-942A-2 | Sequence 2, Appl1 |
| 21 | 900 | 29.1 | 524 | 4 US-09-237-325-2 | Sequence 2, Appl1 |
| 22 | 899 | 29.1 | 544 | 3 US-08-559-397A-19 | Sequence 19, Appl |
| 23 | 894 | 28.9 | 506 | 1 US-08-359-780-2 | Sequence 2, Appl1 |
| 24 | 894 | 28.9 | 506 | 1 US-08-475-682-2 | Sequence 2, Appl1 |
| 25 | 894 | 28.9 | 506 | 1 US-08-780-833-2 | Sequence 2, Appl1 |
| 26 | 894 | 28.9 | 506 | 1 US-08-636-036-2 | Sequence 2, Appl1 |
| 27 | 894 | 28.9 | 506 | 3 US-08-918-509-2 | Sequence 2, Appl1 |

ALIGNMENTS

| | | | | | |
|----|-------|------|-----|------------------------|--------------------|
| 28 | 894 | 28.9 | 506 | 3 US-09-108-262-2 | Sequence 2, Appl1 |
| 29 | 894 | 28.9 | 506 | 4 US-09-688-188B-94 | Sequence 94, Appl |
| 30 | 894 | 28.9 | 506 | 4 US-09-291-417D-94 | Sequence 94, Appl |
| 31 | 893.5 | 28.9 | 551 | 4 US-09-949-016-10951 | Sequence 10951, A |
| 32 | 892.5 | 28.9 | 545 | 4 US-09-538-092-1297 | Sequence 1297, Ap |
| 33 | 891.5 | 28.9 | 545 | 2 US-08-935-760-4 | Sequence 4, Appl1 |
| 34 | 891.5 | 28.9 | 545 | 4 US-09-688-188B-93 | Sequence 93, Appl |
| 35 | 891.5 | 28.9 | 545 | 4 US-09-291-417D-93 | Sequence 93, Appl |
| 36 | 867 | 28.1 | 544 | 3 US-08-559-397A-29 | Sequence 29, Appl |
| 37 | 849 | 27.5 | 544 | 3 US-08-559-397A-30 | Sequence 30, Appl |
| 38 | 833.5 | 27.0 | 465 | 2 US-08-114-555A-2 | Sequence 2, Appl1 |
| 39 | 821 | 26.6 | 694 | 3 US-08-559-397A-31 | Sequence 31, Appl1 |
| 40 | 814.5 | 26.4 | 465 | 3 US-08-559-397A-2 | Sequence 2, Appl1 |
| 41 | 804 | 26.0 | 305 | 4 US-09-765-815-10 | Sequence 10, Appl |
| 42 | 793 | 25.3 | 793 | 3 US-09-588-256-10 | Sequence 10, Appl |
| 43 | 769 | 24.9 | 268 | 2 US-08-852-743-3 | Sequence 3, Appl1 |
| 44 | 769 | 24.9 | 268 | 3 US-09-185-370-3 | Sequence 3, Appl1 |
| 45 | 755 | 24.4 | 410 | 4 US-09-248-796A-18461 | Sequence 18461, A |

RESULT 1
US-09-082-737-2
Sequence 2, Application US/09082737
Patent No. 6013500
GENERAL INFORMATION:
APPLICANT: Minden, Audrey
TITLE OF INVENTION: PAK4, A No. 6013500e1 Gene Encoding A Serine/
TITLE OF INVENTION: Threonine Kinase
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESSES:
ADDRESSER: Cooper & Dunham LLP
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 11230
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/082,737
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 0575/55311
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
TELEFAX: (212) 391-0525
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 591 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-082-737-2
Query Match 100.0%; Score 3090; DB 3; Length 591;
Best Local Similarity 100.0%; Pred. No. 36-191;
Matches 591; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MFGRKKRVRISAPSNPEHRVHTGPOHREKFTGLPRQOSLIBESARRKXPLVDPACIT 60
DB 1 MFGRKKRVRISAPSNPEHRVHTGPOHREKFTGLPRQOSLIBESARRKXPLVDPACIT 60
QY 61 SIQGA PKTVRSKAKDGLTLLDPEFNMGVTRSNLSRRDSPPPARARQENGPEE 120

Db 61 SIOPGAPKTIVRGSKGAKDGLATLLDDEFENMSTVTRNSLRRDSPPPARARQENGMPEE 120
Qy 121 PATTARGPAGKASRGGRFAGHSEAGGSGDRRRAGPEKRPKSSRESGGSGPQESSRDRKPL 180
Db 121 PATTARGPAGKASRGGRFAGHSEAGGSGDRRRAGPEKRPKSSRESGGSGPQESSRDRKPL 180
Qy 181 SGPDVGTPOGAGLASGAKLAAGRPFNTYPRADTDHPSRGAQGEPHDVA PNGPSAGLAIP 240
Db 181 SGPDVGTPOGAGLASGAKLAAGRPFNTYPRADTDHPSRGAQGEPHDVA PNGPSAGLAIP 240
Qy 241 QSSSSSSRPPTRRAGAPSPGVLPAGHASEPQLAPACTPAA PAVGPPGPSPOREPQVRS 300
Db 241 QSSSSSSRPPTRRAGAPSPGVLPAGHASEPQLAPACTPAA PAVGPPGPSPOREPQVRS 300
Qy 301 HEQFRALQLVDPGDRSYLDNFIKIGESTGIVCIATVRSSGKLVAVKMDLRKQORR 360
Db 301 HEQFRALQLVDPGDRSYLDNFIKIGESTGIVCIATVRSSGKLVAVKMDLRKQORR 360
Qy 361 ELLEFNEVIMRDYOHENVMNYSYLVGDELMVMEFLGEGALTDIYTHTRMNEEQIAAV 420
Db 361 ELLEFNEVIMRDYOHENVMNYSYLVGDELMVMEFLGEGALTDIYTHTRMNEEQIAAV 420
Qy 421 CLAVLQALSVLHAQGVTHRDIKSDSILLTHDGRVKLSDFGCQVSKVPRRKSIVGTPT 480
Db 421 CLAVLQALSVLHAQGVTHRDIKSDSILLTHDGRVKLSDFGCQVSKVPRRKSIVGTPT 480
Qy 481 WMAPELISRLPYGEBVDIWSLGIWVEMVDEPPYFNEPPLKAMKMRDNLPRLLKXILHK 540
Db 481 WMAPELISRLPYGEBVDIWSLGIWVEMVDEPPYFNEPPLKAMKMRDNLPRLLKXILHK 540
Qy 541 VSPSLKGFRLRLVDRDPAQRATAELKHPFLAKAGPASIIVPLMRQNRTR 591
Db 541 VSPSLKGFRLRLVDRDPAQRATAELKHPFLAKAGPASIIVPLMRQNRTR 591

RESULT 2
US-09-688-103
; Sequence 103, Application US/09688188B
; Patent No. 6656716
; GENERAL INFORMATION:
; APPLICANT: PLOMMAN, GREGORY
; APPLICANT: MARTINEZ, RICARDO
; APPLICANT: WHITE, DAVID
; TITLE OF INVENTION: STE20-RELATED PROTEIN KINASES
; PILE REFERENCE: 038602/0328
; CURRENT APPLICATION NUMBER: US/09/688, 1888
; CURRENT FILING DATE: 2000-10-16
; PRIOR APPLICATION NUMBER: 09/291,417
; PRIOR FILING DATE: 1999-04-14
; PRIOR APPLICATION NUMBER: 60/081,784
; PRIOR FILING DATE: 1998-04-14
; NUMBER OF SEQ ID NOS: 155
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 103
; LENGTH: 591
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-688-188B-103

Query Match 100.0%; Score 3090; DB 4; Length 591;
Best Local Similarity 100.0%; Pred. No. 3e-191;
Matches 591; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MFGRRKRRVEISAPSNFEHRVHTGFDQHEQKFTGLPRQWOSLIBESARRPKPLVDPACT 60
Db 1 MFGRRKRRVEISAPSNFEHRVHTGFDQHEQKFTGLPRQWOSLIBESARRPKPLVDPACT 60
Qy 61 SIOPGAPKTIVRGSKGAKDGLATLLDDEFENMSTVTRNSLRRDSPPPARARQENGMPEE 120
Db 61 SIOPGAPKTIVRGSKGAKDGLATLLDDEFENMSTVTRNSLRRDSPPPARARQENGMPEE 120
Qy 121 PATTARGPAGKASRGGRFAGHSEAGGSGDRRRAGPEKRPKSSRESGGSGPQESSRDRKPL 180
Db 121 PATTARGPAGKASRGGRFAGHSEAGGSGDRRRAGPEKRPKSSRESGGSGPQESSRDRKPL 180

Db 121 PATTARGPAGKASRGGRFAGHSEAGGSGDRRRAGPEKRPKSSRESGGSGPQESSRDRKPL 180
Qy 181 SGPDVGTPOGAGLASGAKLAAGRPFNTYPRADTDHPSRGAQGEPHDVA PNGPSAGLAIP 240
Db 181 SGPDVGTPOGAGLASGAKLAAGRPFNTYPRADTDHPSRGAQGEPHDVA PNGPSAGLAIP 240
Qy 241 QSSSSSSRPPTRRAGAPSPGVLPAGHASEPQLAPACTPAA PAVGPPGPSPOREPQVRS 300
Db 241 QSSSSSSRPPTRRAGAPSPGVLPAGHASEPQLAPACTPAA PAVGPPGPSPOREPQVRS 300
Qy 301 HEQFRALQLVDPGDRSYLDNFIKIGESTGIVCIATVRSSGKLVAVKMDLRKQORR 360
Db 301 HEQFRALQLVDPGDRSYLDNFIKIGESTGIVCIATVRSSGKLVAVKMDLRKQORR 360
Qy 361 ELLEFNEVIMRDYOHENVMNYSYLVGDELMVMEFLGEGALTDIYTHTRMNEEQIAAV 420
Db 361 ELLEFNEVIMRDYOHENVMNYSYLVGDELMVMEFLGEGALTDIYTHTRMNEEQIAAV 420
Qy 421 CLAVLQALSVLHAQGVTHRDIKSDSILLTHDGRVKLSDFGCQVSKVPRRKSIVGTPT 480
Db 421 CLAVLQALSVLHAQGVTHRDIKSDSILLTHDGRVKLSDFGCQVSKVPRRKSIVGTPT 480
Qy 481 WMAPELISRLPYGEBVDIWSLGIWVEMVDEPPYFNEPPLKAMKMRDNLPRLLKXILHK 540
Db 481 WMAPELISRLPYGEBVDIWSLGIWVEMVDEPPYFNEPPLKAMKMRDNLPRLLKXILHK 540
Qy 541 VSPSLKGFRLRLVDRDPAQRATAELKHPFLAKAGPASIIVPLMRQNRTR 591
Db 541 VSPSLKGFRLRLVDRDPAQRATAELKHPFLAKAGPASIIVPLMRQNRTR 591

RESULT 3
US-09-718-032-2
; Sequence 2, Application US/09718032
; Patent No. 6667168
; GENERAL INFORMATION:
; APPLICANT: The Trustees of Columbia University
; APPLICANT: Minden, Audrey
; TITLE OF INVENTION: PAK4, A NOVEL GENE ENCODING A SERINE/THREONINE KINASE
; PILE REFERENCE: 575/55311-A-PCT-US
; CURRENT APPLICATION NUMBER: US/09/718, 032
; CURRENT FILING DATE: 2000-11-21
; PRIOR APPLICATION NUMBER: PCT/US99/11341
; PRIOR FILING DATE: 1999-05-21
; PRIOR APPLICATION NUMBER: 09/082,737
; PRIOR FILING DATE: 1998-05-21
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 591
; TYPE: PRT
; ORGANISM: human
US-09-718-032-2

Query Match 100.0%; Score 3090; DB 4; Length 591;
Best Local Similarity 100.0%; Pred. No. 3e-191;
Matches 591; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MFGRRKRRVEISAPSNFEHRVHTGFDQHEQKFTGLPRQWOSLIBESARRPKPLVDPACT 60
Db 1 MFGRRKRRVEISAPSNFEHRVHTGFDQHEQKFTGLPRQWOSLIBESARRPKPLVDPACT 60
Qy 61 SIOPGAPKTIVRGSKGAKDGLATLLDDEFENMSTVTRNSLRRDSPPPARARQENGMPEE 120
Db 61 SIOPGAPKTIVRGSKGAKDGLATLLDDEFENMSTVTRNSLRRDSPPPARARQENGMPEE 120
Qy 121 PATTARGPAGKASRGGRFAGHSEAGGSGDRRRAGPEKRPKSSRESGGSGPQESSRDRKPL 180
Db 121 PATTARGPAGKASRGGRFAGHSEAGGSGDRRRAGPEKRPKSSRESGGSGPQESSRDRKPL 180
Qy 181 SGPDVGTPOGAGLASGAKLAAGRPFNTYPRADTDHPSRGAQGEPHDVA PNGPSAGLAIP 240
Db 181 SGPDVGTPOGAGLASGAKLAAGRPFNTYPRADTDHPSRGAQGEPHDVA PNGPSAGLAIP 240